```
              GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:   January  6, 2003, 12:46:55 ; Search time 28.5758 Seconds
                                        (without alignments)
                                        573.557 Million cell updates/sec

Title:          US-09-155-739-11
Perfect score:  655
Sequence:       1 QVQLVQSGAEVKKPGASVKV.........NVGVYAMDYWGQGTLVTVSS 123

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:        908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	655	100.0	123	16	AAR81323	Humanized VLA-4 an
2	655	100.0	142	16	AAR81333	Human VLA-4 reshap
3	655	100.0	142	18	AAW22428	Humanised alpha-4
4	648	98.9	123	18	AAW22413	Humanised alpha-4
5	552	84.3	123	16	AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16	AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18	AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19	AAW44124	Heavy chain variab
9	523.5	79.9	120	23	AAU79034	Humanised antibody
10	523.5	79.9	431	22	AAB30693	A fusion of single
11	523	79.8	136	16	AAR76681	Human/murine chime
12	523	79.8	136	17	AAW04396	Chimaeric human/mu
13	523	79.8	269	16	AAR76682	Human ONS-M21 anti
14	523	79.8	269	17	AAW04397	Chimaeric human/mu
15	515	78.6	269	16	AAR81325	Humanized VLA-4 an
16	515	78.6	119	18	AAW22426	Humanised alpha-4
17	512	78.2	119	16	AAR81324	Humanized VLA-4 an
18	512	78.2	135	18	AAW22425	Humanised alpha-4
19	507.5	77.5	135	21	AAW07969	A heavy chain vari
20	505.5	77.2	258	23	ABB05963	Monoclonal antibod
21	505.5	77.2	258	23	ABB05992	Mouse and human ch
22	505.5	77.2	258	23	ABB05996	Human monoclonal a
23	504.5	77.0	118	14	AAR37611	hIL2R Ab H chain V
24	503	76.8	119	20	AAY52717	Humanised ATR-5 H
25	503	76.8	119	22	AAB74978	Humanised ATR-5 H
26	501.5	76.6	258	23	ABB05991	Mouse and human ch
27	501.5	76.6	258	23	ABB05995	Human monoclonal a
28	499	76.2	119	20	AAY52719	Humanised ATR-5 H
29	499	76.2	119	22	AAB74980	Humanised ATR-5 H
30	496	75.7	136	17	AAR92084	Humanised antibody
31	495	75.6	119	16	AAR81331	Human 2*CL antibod
32	493	75.3	119	20	AAY52718	Humanised ATR-5 H
33	493	75.3	119	22	AAB74979	Humanised ATR-5 H
34	492	75.1	117	15	AAR57476	CDR-grafted anti-R
35	492	75.1	117	17	AAR92079	Murine 1308F VH CD
36	492	75.1	136	15	AAR57481	Humanized 1308F VH
37	491.5	75.0	245	23	ABP45885	Human BLyS binding
38	491	75.0	119	20	AAY52708	Humanised ATR-5 H
39	491	75.0	119	22	AAB74969	Humanised ATR-5 H
40	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
41	489	74.7	119	20	AAY52720	Humanised ATR-5 H
42	489	74.7	119	22	AAB74981	Humanised ATR-5 H
43	487.5	74.4	120	15	AAR47491	Humanised anti-CD1
44	487.5	74.4	258	23	ABB05993	Mouse and human ch
45	487.5	74.4	258	23	ABB05997	Human monoclonal a

ALIGNMENTS

```
RESULT 1
AAR81323
ID   AAR81323 standard; Protein; 123 AA.
XX
AC   AAR81323;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
```

PS   Claim 11; Page 69; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence 123 AA;

Query Match   100.0%; Score 655; DB 16; Length 123;
Best Local Similarity   100.0%; Pred. NO. 6.6e-53;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy   121 VSS 123
            |||
Db   121 VSS 123

RESULT 2
AAR81333
ID   AAR81333 standard; Protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /note= "signal peptide"
FT   Region   20..49
FT   /note= "framework region 1"
FT   Region   50..54
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /note= "framework region 2"
FT   Region   69..85
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /note= "framework region 3"
FT   Region   118..131
FT   /note= "complementarity determining region 3"
FT   Region   132..142
FT   /note= "framework region 4"
XX

PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions. In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence 142 AA;

Query Match   100.0%; Score 655; DB 16; Length 142;
Best Local Similarity   100.0%; Pred. No. 7.8e-53;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db   80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy   121 VSS 123
            |||
Db   140 VSS 142

RESULT 3
AAW22428
ID   AAW22428 standard; Protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;

KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= Leader
FT   Protein   20..142
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FT   /note= "VH version Ha (Claim 25)"
FT   Region   20..49
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FT   /note= "21/28'CL framework region 1"
FT   Region   50..55
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   55..67
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FT   /note= "21/28'CL framework region 2"
FT   Region   68..85
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "21/28'CL framework region 3"
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FT   /label= FR4
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413). It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW24212) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   142 AA;

Query Match   100.0%; Score 655; DB 18; Length 142;
Best Local Similarity   100.0%; Pred. No. 7.8e-53;
Matches   123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db   80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy 121 VSS 123
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Db 140 VSS 142

RESULT 4
AAW22413
ID   AAW22413 standard; Protein; 123 AA.
XX
AC   AAW22413;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
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FT   /note= "21/28'CL framework region 1"
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FT   /note= "21/28'CL residues 27-30 are replaced by
FT   those of MAB 21.6, involved in antigen
FT   binding"
FT   Region   31..35
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   36..49
FT   /label= FR2
FT   /note= "21/28'CL framework region 2"
FT   Region   50..66
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   67..98
FT   /label= FR3
FT   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT   21.6 VL, important in supporting the CDR2
FT   loop"
FT   Region   99..112
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FT   /note= "21.6 complementarity determining region 3"
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.

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XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 7; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VH
CC   region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human 21/28'CL framework. It can be expressed
CC   in mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence  123 AA;

Query Match             98.9%;  Score 648;  DB 18;  Length 123;
Best Local Similarity   99.2%;  Pred. No. 2.9e-52;
Matches  122;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

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Db      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy    121 VSS 123
          |||
Db    121 VSS 123


RESULT 5
AAR81330
ID   AAR81330 standard; Protein; 123 AA.
XX
AC   AAR81330;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW   Humanised antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
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FT                   /label= FR1
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PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
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PR   25-JAN-1994;   94US-0186269.
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PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 68; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (see AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  123 AA;

Query Match             84.3%;  Score 552;  DB 16;  Length 123;
Best Local Similarity   82.9%;  Pred. No. 2e-43;
Matches  102;  Conservative  11;  Mismatches  10;  Indels   0;  Gaps   0:

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
```

/note= "mouse heavy chain variable framework
region 1"

/note= "mouse heavy chain variable complementarity
determining region 1"

/note= "mouse heavy chain variable framework
region 2"

/note= "mouse heavy chain variable complementarity
determining region 2"

/note= "mouse heavy chain variable framework
region 3"

/note= "mouse heavy chain variable complementarity
determining region 3"

/note= "mouse heavy light chain variable framework
region 4"

```
Db      :||| |||||| ||||||| :||:|||:|:||||||||||
      1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60
Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         ||||||: ||||||||::||||:||||| |||||||||||||||||||||||||| |
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120
Qy  121 VSS 123
         |||
Db  121 VSS 123

RESULT 6
AAR81327
ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VlA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /note= "signal peptide"
FT   Region         20..49
FT                  /note= "framework region 1"
FT   Region         50..54
FT                  /note= "complementarity determining region 1"
FT   Region         55..68
FT                  /note= "framework region 2"
FT   Region         69..85
FT                  /note= "complementarity determining region 2"
FT   Region         86..117
FT                  /note= "framework region 3"
FT   Region         118..131
FT                  /note= "complementarity determining region 3"
FT   Region         132..140
FT                  /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB: AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  140 AA;

Query Match             83.1%;  Score 544;  DB 16;  Length 140;
Best Local Similarity   82.6%;  Pred. No. 1.3e-42;
Matches 100;  Conservative 11;  Mismatches 10;  Indels 0;  Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         :||| |||||| |||||||||: ||||| ||||||: ||:|:|||||||||||||||||
Db   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         ||||||: ||||||||::||||:||||||||||||||||||||||||||||||| |
Db   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
Qy  121 V 121
          |
Db  140 V 140

RESULT 7
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /label= Leader
FT   Region         20..49
FT                  /label= FR1
FT                  /note= "framework region 1"
FT   Region         50..54
FT                  /label= CDR1
FT                  /note= "complementarity determining region 1"
FT   Region         55..68
FT                  /label= FR2
FT                  /note= "framework region 2"
FT   Region         69..85
FT                  /label= CDR2
FT                  /note= "complementarity determining region 2"
FT   Region         86..117
FT                  /label= FR3
FT                  /note= "framework region 3"
FT   Region         118..131
FT                  /label= CDR3
FT                  /note= "complementarity determining region 3"
FT   Region         132..140
FT                  /label= FR4
FT
```

```
FT                    /note= "framework region 4"
XX
PN    WO9718838-A1.
XX
PD    29-MAY-1997.
XX
PF    21-NOV-1996;  96WO-US18807.
XX
PR    21-NOV-1995;  95US-0561521.
XX
PA    (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI    Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR    WPI; 1997-297879/27.
DR    N-PSDB; AAT74760.
XX
PT    Uses of humanised alpha-4 integrin antibody - for treatment of
PT    asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS    Claim 18; Page 69-70; 107pp; English.
XX
CC    This polypeptide comprises the heavy chain variable region (VH) of
CC    mouse anti-alpha-4 integrin monoclonal antibody 21.6.  The
CC    complementarity determining regions (CDRs) of the 21.6 VH can be
CC    incorporated into a human 21/28'CL framework to produce a claimed
CC    humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC    antibody that is used in the manufacture of a medicament for
CC    treating a disease selected from asthma, atherosclerosis, AIDS,
CC    dementia, diabetes, inflammatory bowel disease, rheumatoid
CC    arthritis, transplant rejection, graft versus host disease, tumour
CC    metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC    ischaemia, and acute leukocyte mediated lung injury.  The antibody
CC    may also be used in the affinity purification of alpha-4 integrin
CC    for use as a vaccine or an immunogen.  It is also useful for
CC    generating idiotypic antibodies.  The humanised antibodies of the
CC    invention have a half-life in the human circulation essentially
CC    equivalent to that of naturally occurring human antibodies.
XX
SQ    Sequence 140 AA;

Query Match    83.1%;  Score 544;  DB 18;  Length 140;
Best Local Similarity  82.6%;   Pred. No. 1.3e-42;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        :||:|||||:|||||||||:||||||||| : |: :|||:||||||||||||||||
Db   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        |||||:|:|||||| |||||||::||||||||||||||||||:||||||||||||||||
Db   80 DPKFQGKATITADTSSNTAYLQ:SSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy  121 V 121
        |
Db  140 V 140

RESULT 8
AAW44124
ID   AAW44124 standard; Protein; 120 AA.
XX
AC   AAW44124;
XX
DT   05-JUN-1998  (first entry)
XX
DE   Heavy chain variable region of humanised NR-LU-13 antibody NRX451.
XX
KW   Heavy chain; variable region; murine; mouse; human; cancer antigen;
KW   antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
KW   treatment.
XX
OS   Mus sp.
```

```
OS   Synthetic.
.;
FH   Key            Location/Qualifiers
FT   Region         31..35
FT                  /note= "complementarity determining region 1"
FT   Region         50..59
FT                  /note= "complementarity determining region 2"
FT   Region         99..109
FT                  /note= "complementarity determining region 3"
XX
PN    WO9746589-A2.
XX
PD    11-DEC-1997.
XX
PF    06-JUN-1997;  97WO-US10074.
XX
PR    07-JUN-1996;  96US-0660362.
XX
PA    (NEOR-) NEORX CORP.
XX
PI    Graves SS, Henry AH, Hylarides MD, Mallet RW, Pedersen JT;
PI    Rees AR, Renojm, Searle SMJ;
XX
DR    WPI; 1998-042124/04.
XX
PT    Humanised antibody binds same human cancer antigen as antibody
PT    NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT    therapy and immunodiagnosis
XX
PS    Example 1; Fig 4; 100pp; English.
XX
CC    The present sequence is the heavy chain variable region of the
CC    humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
CC    NRX451.
CC    A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC    hAb, specifically NRX451, or its conjugates can be used for the
CC    manufacture of a diagnostic or medicament for cancer diagnosis or
CC    treatment. The hAb has reduced immunogenicity and toxicity in
CC    humans, but retains the ability to bind the NR-LU-13 antigen.
XX
SQ    Sequence  120 AA;

Query Match    79.9%;   Score 523.5;  DB 19;  Length 120;
Best Local Similarity  82.9%;   Pred. No. 8.3e-41;
Matches 102; Conservative  8; Mismatches 10; Indels  3;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||||||||||||||||||||||||||:|||||||||| |::||||||||:|||
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKC 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        | |||||||||||:||||||||||||||||||||::|||:||| :::||||||||||||
Db   61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117

Qy  121 VSS 123
        |||
Db  118 VSS 120

RESULT 9
AAU79034
ID   AAU79034 standard; Protein; 120 AA.
XX
AC   AAU79034;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Humanised antibody NRX451 heavy chain variable region.
XX
KW   Mouse; NR-LU-13; humanised antibody; NRX451; cancer;
KW   cytostatic; heavy chain variable region; human.
XX
OS   Mus sp.
```

```
OS   Homo sapiens.
XX
PN   WO200075333-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000;  2000WO-US15595.
XX
PR   07-JUN-1999;    99US-0137900.
PR   03-DEC-1999;    99US-0168976.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Goshorn SC,  Graves SS,  Schultz JE,  Lin Y,  Sanderson JA,  Reno JM;
XX
DR   WPI; 2001-091213/10.
DR   N-PSDB; AAC86562.
XX
PT   New vector constructs for expressing genomic streptavidin fusion
PT   proteins which are useful for targeting tumour cells associated with
PT   cancer, e.g. adenocarcinomas -
XX
PS   Example 1; Fig 10; 100pp; English.
XX
CC   The present sequence encodes a fusion of the single chain antibody
CC   huNR-LU-10 and streptavidin. The antibody binds the antigen EGP40 or
CC   EPCAM. The fusion protein is expressed using vectors of the invention.
CC   The specification describes vector constructs for expressing streptavidin
CC   fusion proteins. The vector comprises a first nucleic acid encoding
CC   streptavidin or its functional variant operatively linked to a promoter,
CC   and a cloning site for insertion of a second nucleic acid sequence
CC   encoding a polypeptide to be fused with streptavidin, interposed between
CC   the promoter and the first nucleic acid sequence. Alternatively, the
CC   vector construct comprises a first nucleic acid, operatively linked to a
CC   promoter, encoding a polypeptide to be fused with streptavidin, and a
CC   cloning site for insertion of a second nucleic acid encoding at least
CC   129 amino acids of streptavidin or its functional variant. The fusion
CC   proteins are useful for targeting tumour cells, particularly tumour cells
CC   associated with cancer, e.g. adenocarcinomas or hematological
CC   malignancies. The vector construct is useful for expressing of
CC   streptavidin fusion proteins. In particular, these are useful as tools
CC   for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC   presence or absence of, or treating, a target site within a mammalian
CC   host.
XX
SQ   Sequence  431 AA;

Query Match             79.9%;  Score 523.5;  DB 22;  Length 431;
Best Local Similarity   82.9%;  Pred. No. 3.4e-40;
Matches 102;  Conservative   8;  Mismatches  10;  Indels  3;  Gaps  1;

Qy     1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
          |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   148  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKS  207

Qy    61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
          |||||||||||||||||||||||||||||:|||||||||||||| ::|||||||||||
Db   208  DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT  264

Qy   121  VSS  123
          |||
Db   265  VSS  267
```

RESULT 11
```
AAR76681
ID   AAR76681 standard; Protein; 136 AA.
XX
AC   AAR76681;
XX
DT   17-JAN-1996  (first entry)
XX
DE   Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
```

```
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US635B710-B1.
XX
PD   19-MAR-2002.
XX
PF   09-JUN-1997;    97US-0871488.
XX
PR   07-JUN-1996;    96US-0660362.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Graves SS,  Reno JM, Mallett RW,  Hylarides MD,  Searle SMJ;
PI   Henry AH,  Pedersen JT,  Rees AR;
XX
DR   WPI; 2002-314754/35.
XX
PT   Humanised antibody NRX-451, which is derived from ATCC CRL-12360, but
PT   which has reduced immunogenicity or toxicity, useful for diagnosing and
PT   treating cancers -
XX
PS   Claim 1; Fig 4; 53pp; English.
XX
CC   The invention relates to the humanised antibody NRX 451 (or an antigen-
CC   binding fragment), in which the murine parent antibody is ATCC CRL-12360
CC   (also known as NU-LU-13 which targets a 40 kilodalton glycoprotein
CC   expressed by many carcinomas) and which comprises the light chain
CC   variable region appearing as AAU79033 and the heavy chain variable region
CC   appearing as AAU79034. The antibody may be administered to treat cancers
CC   and use to detect the presence of the antigen in clinical samples.
CC   The antibody is a humanised antibody derived from NR-LU-13
CC   antibodies, which exhibits reduced immunogenicity or toxicity in humans
CC   but retains the ability to bind the NR-LU-13 antigen. The antibody
CC   either does not possess N-linked glycosylation or its N-linked
CC   glycosylation has been modified post expression to reduce
CC   immunogenicity or toxicity. The present sequence represents the heavy
CC   chain variable region of humanised antibody of the invention, NRX451.
XX
SQ   Sequence  120 AA;

Query Match             79.9%;  Score 523.5;  DB 23;  Length 120;
Best Local Similarity   82.9%;  Pred. No. 8.3e-41;
Matches 102;  Conservative   8;  Mismatches  10;  Indels  3;  Gaps  1;

Qy     1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
          |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db     1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQGLQWMGRIDPANGNTKC  60

Qy    61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
          |||||||||||||||||||||||||||||:|||||||||||| | :::|||||||||||
Db    61  DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT  117

Qy   121  VSS  123
          |||
Db   118  VSS  120
```

RESULT 10
```
AAB30693
ID   AAB30693 standard; Protein; 431 AA.
XX
AC   AAB30693;
XX
DT   02-APR-2001  (first entry)
XX
DE   A fusion of single chain antibody/streptavidin.
XX
KW   Streptavidin; tumour cell; cancer; adenocarcinoma;
KW   hematological malignancy; huNR-LU-10; EGP40; EPCAM.
XX
OS   Synthetic.
OS   Streptomyces avidinii.
```

```
XX
KW   Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..50
FT                   /label= FR 1
FT   Peptide         51..55
FT                   /label= CDR 1
FT   Peptide         56..59
FT                   /label= FR 2
FT   Peptide         70..86
FT                   /label= CDR 2
FT   Peptide         87..118
FT                   /label= FR 3
FT   Peptide         119..126
FT                   /label= CDR 3
FT   Peptide         127..136
FT                   /label= FR 4
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94539.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 26; Page 94; 120pp; Japanese.
XX
CC   AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-
CC   RVL-M21g(gamma)1. The antibody is reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   136 AA;

Query Match             79.8%;   Score 523;  DB 16;  Length 136;
Best Local Similarity   83.7%;   Pred. No. 1.1e-40;
Matches  103; Conservative   4; Mismatches  10; Indels   6; Gaps    2;

Qy     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||||||||||||||||||||||||||||:||||| ||
Db    20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79

Qy    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||||||||| |:|||||||||||||||||||||| ||   |||||| ||
Db    80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133

Qy   121 VSS 123
         |||
Db   134 VSS 136

RESULT 12
AAW04396
ID   AAW04396 standard; Protein; 136 AA.
XX
AC   AAW04396;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..136
FT                   /label= mat_peptide
FT   Region          50..54
FT                   /label= CDR_1
FT   Region          69..85
FT                   /label= CDR_2
FT   Region          118..125
FT                   /label= CDR_3
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38653.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 5; Pages 38-39; 45pp; Japanese.
XX
CC   The present sequence is a fragment of the chimaeric human/murine
CC   monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by
CC   combining light and heavy variable region DNA, from a murine
CC   anti-human myeloblastoma cell MAb, with human light and heavy
CC   constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

Query Match             79.8%;   Score 523;  DB 17;  Length 136;
Best Local Similarity   83.7%;   Pred. No. 1.1e-40;
Matches  103; Conservative   4; Mismatches  10; Indels   6; Gaps    2;

Qy     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||||||||||||||||||||||||||||:||||| ||
Db    20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79

Qy    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||||||||| |:|||||||||||||||||||||||| ||   |||||| ||
Db    80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133
```

Qy   121 VSS 123
          |||
Db   134 VSS 136

RESULT 13
AAR76682
ID   AAR76682 standard; Protein; 269 AA.
XX
AC   AAR76682;
XX
DT   18-JAN-1996 (first entry)
XX
DE   Human ONS-M21 antibody Fv fragment.
XX
KW   Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..22
FT   /label= sig_peptide
FT   Region   23..139
FT   /note="heavy variable region"
FT   Region   140..154
FT   /note="linker"
FT   Region   155..269
FT   /note="light variable region"
FT   Region   262..269
FT   /note="FLAG"
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PN   WO9514041-A1.
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PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94548.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 35; Pages 98-99; 120pp; Japanese.
XX
CC   AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the
CC   human antibody ONS-M21 Fv fragment. The plasmid was used in the
CC   construction of an expression vector, contg. cDNA encoding a
CC   human/murine chimeric antibody, reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   269 AA;

Query Match   79.8%;   Score 523; DB 16; Length 269;
Best Local Similarity 83.7%;   Pred. No. 2.2e-40;
Matches 103;   Conservative   4;   Mismatches   10;   Indels   6;   Gaps

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db   23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNTGVYAMDYWGQGTLVT 120
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Db   83 DPKFQGRVTITADESNTAYMELSSLRSEDTAFYFCA-SAYYVN----QDYWGQGTTVT 136

Qy   121 VSS 123
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Db   137 VSS 139

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ID   AAW04397 standard; Protein; 269 AA.
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AC   AAW04397;
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DT   09-DEC-1996 (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 scFv fragment.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..22
FT   /label= sig_peptide
FT   Region   23..139
FT   /note="heavy variable region"
FT   Peptide   140..154
FT   /label= linker
FT   Region   155..261
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FT   /label= FLAG
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PN   JP08169900-A.
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PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
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PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38662.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma.
XX
PS   Example 6; Pages 40-41; 45pp; Japanese.
XX
CC   The present sequence is a scFv fragment from the chimaeric
CC   human/murine monoclonal antibody (MAB) ONS-M21. The MAb was
CC   prepd. by combining light and heavy variable region DNA, from a
CC   murine anti-human myeloblastoma cell MAb, with human light and
CC   heavy constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   269 AA;

Query Match   79.8%;   Score 523; DB 17; Length 269;
Best Local Similarity 83.7%;   Pred. No. 2.2e-40;

Matches 103;   Conservative   4;   Mismatches   10;   Indels   6;   Gaps   2;

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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy  121 VSS 123
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Db  137 VSS 139
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Matches 102;   Conservative   5;   Mismatches   12;   Indels   4;   Gaps   1;

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Qy  121 VSS 123
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Db  117 VSS 119
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Job time : 29.5758 secs

RESULT 15
AAR81325
ID   AAR81325 standard; Protein; 119 AA.
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AC   AAR81325;
XX
DT   02-APR-1996 (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 13; Page 70; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence 119 AA;

Query Match   78.6%;   Score 515; DB 16; Length 119;
Best Local Similarity   82.9%;   Pred. No. 5e-40;

GenCore version 5.1.3

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OM protein - protein search, using sw model

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355.228 Million cell updates/sec

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Perfect score: 655
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	2	US-08-561-521-11	Sequence 11, Appl
2	655	100.0	123	2	PCT-US95-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appl
6	552	84.3	123	5	PCT-US95-01219-9	Sequence 9, Appli
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appl
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appli
9	523.5	79.9	120	4	US-08-871-488A-19	Sequence 19, Appl
10	523	79.8	117	4	US-08-646-265A-132	Sequence 132, App
11	523	79.8	136	4	US-08-646-265A-99	Sequence 99, Appl
12	523	79.8	269	4	US-08-646-265A-109	Sequence 109, App
13	515	78.6	119	5	US-08-561-521-13	Sequence 13, Appl
14	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
15	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
16	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appli
17	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
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19	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
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21	492	75.1	117	5	US-08-290-592E-17	Sequence 17, Appl
22	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
23	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
24	492	75.1	119	4	US-09-438-954-41	Sequence 41, Appl
25	491.5	75.0	118	2	US-08-232-081B-8	Sequence 8, Appli
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28	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
29	484.5	74.0	135	2	US-08-137-117D-112	Sequence 112, App
30	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
31	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
32	484.5	74.0	139	3	US-08-452-164A-19	Sequence 19, Appl
33	484.5	74.0	139	3	US-08-603-024-18	Sequence 18, Appl
34	481	73.4	121	1	US-08-202-047-23	Sequence 23, Appl
35	481	73.4	121	3	US-08-964-690-23	Sequence 23, Appl
36	480.5	73.4	124	4	US-09-301-593-16	Sequence 16, Appl
37	480.5	73.4	124	4	US-09-301-593-41	Sequence 41, Appl
38	475	72.5	119	4	US-09-438-954-4	Sequence 4, Appli
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40	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
41	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
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ALIGNMENTS

RESULT 1
US-08-561-521-11

; Sequence 11, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-11

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Best Local Similarity   100.0%; Pred. No. 1.4e-58;
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RESULT 2
PCT-US95-01219-11
; Sequence 11, Application PCT/US9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-11

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Best Local Similarity  100.0%;  Pred. No. 1.4e-58;  Indels 0;  Gaps 0;
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Qy  121 VSS 123
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Db  121 VSS 123
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RESULT 3
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-17

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RESULT 4
PCT-US95-01219-17
; Sequence 17, Application PCT/US9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.

```
;       APPLICANT:  Saldanha, Jose
;       APPLICANT:  Jones, S. Tarran
;       TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;       TITLE OF INVENTION:  Adhesion Molecule VLA-4
;       NUMBER OF SEQUENCES:  45
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  Townsend and Townsend Khourie and Crew
;         STREET:  One Market Plaza, Steuart Tower, Suite 2000
;         CITY:  San Francisco
;         STATE:  California
;         COUNTRY:  USA
;         ZIP:  94105
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  PCT/US95/01219
;         FILING DATE:  25-JAN-1995
;         CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:  US 08/186,269
;         FILING DATE:  25-JAN-1994
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Smith, William L.
;         REGISTRATION NUMBER:  30,223
;         REFERENCE/DOCKET NUMBER:  15270-14
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  415-543-9600
;         TELEFAX:  415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  142 amino acids
;         TYPE:  amino acid
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
PCT-US95-01219-17

Query Match             100.0%;  Score 655;  DB 5;  Length 142;
Best Local Similarity   100.0%;  Pred. No. 1.6e-58;
Matches  123;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
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Db         80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 139

Qy        121 VSS 123
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Db        140 VSS 142

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US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;       APPLICANT:  Bendig, Mary M.
;       APPLICANT:  Leger, Olivier J.
;       APPLICANT:  Saldanha, Jose
;       APPLICANT:  Jones, S. Tarran
;       TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;       TITLE OF INVENTION:  Adhesion Molecule VLA-4
;       NUMBER OF SEQUENCES:  45
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  Townsend and Townsend Khourie and Crew
;         STREET:  One Market Plaza, Steuart Tower, Suite 2000
;         CITY:  San Francisco
;         STATE:  California
```

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;         COUNTRY:  USA
;         ZIP:  94105
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  US/08/561,521
;         FILING DATE:
;         CLASSIFICATION:  424
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:  US/08/186,269A
;         FILING DATE:  25-JAN-1994
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Smith, William L.
;         REGISTRATION NUMBER:  30,223
;         REFERENCE/DOCKET NUMBER:  15270-14
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  415-543-9600
;         TELEFAX:  415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  123 amino acids
;         TYPE:  amino acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-561-521-9

Query Match             84.3%;  Score 552;  DB 2;  Length 123;
Best Local Similarity   82.9%;  Pred. No. 2.8e-48;
Matches  102;  Conservative  11;  Mismatches  10;  Indels   0;  Gaps   0;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
              :||||||||:|||||||:|||||||||||||||||||:|:-|:|:||||||||||||||
Db          1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
              ||||||:|||||||:|||:||||:||||:|||||||:|||||||||||||:||||||||||
Db         61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy        121 VSS 123
              |||
Db        121 VSS 123

RESULT 6
PCT-US95-01219-9
; Sequence 9, Application PC/TUS9501219
; GENERAL INFORMATION:
;       APPLICANT:  Bendig, Mary M.
;       APPLICANT:  Leger, Olivier J.
;       APPLICANT:  Saldanha, Jose
;       APPLICANT:  Jones, S. Tarran
;       TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;       TITLE OF INVENTION:  Adhesion Molecule VLA-4
;       NUMBER OF SEQUENCES:  45
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  Townsend and Townsend Khourie and Crew
;         STREET:  One Market Plaza, Steuart Tower, Suite 2000
;         CITY:  San Francisco
;         STATE:  California
;         COUNTRY:  USA
;         ZIP:  94105
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  PCT/US95/01219
;         FILING DATE:  25-JAN-1995
```

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;    CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
; INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-9

  Query Match      84.3%;  Score 552;  DB 5;  Length 123;
  Best Local Similarity  82.9%;  Pred. No. 2.8e-48;
  Matches 102;  Conservative 11;  Mismatches 10;  Indels 0;  Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||  ||||:|||||||||::|||| ||||||||||||||:|:||  :| |||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||| |:||||||::||||| :|||| :|||||| ||||||||||||||||||||| ||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy  121 VSS 123
         |||
Db  121 VSS 123

RESULT 7
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
; INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-4

  Query Match      83.1%;  Score 544;  DB 2;  Length 140;
  Best Local Similarity  82.6%;  Pred. No. 2.1e-47;
  Matches 100;  Conservative 11;  Mismatches 10;  Indels 0;  Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||  ||||:|||||||||::|||| ||||||||||||||:|:||  :| |||||||||
Db   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||| |:||||||::||||| :|||| :|||||| ||||||||||||||||||||| ||
Db   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy  121 V 121
         |
Db  140 V 140

RESULT 8
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
; GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
; INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-4

  Query Match      83.1%;  Score 544;  DB 5;  Length 140;
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Best Local Similarity 82.6%; Pred. No. 2.1e-47;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
         :||| |||||| ||||||| ||||||||||||||:| ||:||||||||||||||
Db  20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||| ||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  80 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy 121 V 121
         |
Db 140 V 140
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RESULT 9
US-08-871-488A-19
; Sequence 19, Application US/08871488A
; Patent No. 6358710
; GENERAL INFORMATION:
; APPLICANT: Graves, Scott S.
; APPLICANT: Reno, John M.
; APPLICANT: Mallett, Robert W.
; APPLICANT: Hylarides, Mark D.
; APPLICANT: Searle, Stephen M.J.
; APPLICANT: Henry, Andrew H.
; APPLICANT: Pedersen, Jan T.
; APPLICANT: Rees, Anthony R.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
; TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
; TITLE OF INVENTION: PRETARGETING METHODS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/871,488A
;   FILING DATE: 09-JUN-1997
;   CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Sharkey Ph.D., Richard G.
;   REGISTRATION NUMBER: 32,629
;   REFERENCE/DOCKET NUMBER: 690022.527C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
US-08-871-488A-19

Query Match 79.9%; Score 523.5; DB 4; Length 120;
Best Local Similarity 82.9%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

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Qy  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
        ||||||||||||||||||||||||||||||||||||:|:||||||:|:||||||||| ||
Db  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQLQWMGRIDPANGNTKC  60

Qy 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db 61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117
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         | |||||||||||| :||||||||||||||:|||||||:: |:::||||||||||
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Qy 121 VSS 123
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Db 118 VSS 120
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RESULT 10
US-08-646-265A-132
; Sequence 132, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,265A
;   FILING DATE: 09-SEP-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP94/01763
;   FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 5-291078
;   FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-265A-132

Query Match 79.8%; Score 523; DB 4; Length 117;
Best Local Similarity 83.7%; Pred. No. 2.1e-45;
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

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Qy  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
        |||||||||||||||:|||||||||||||||||||||||||||:||||||||:| ||
Db  1 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY  60

Qy 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        ||||||||||||||:||||||||||||||||||| ||| |||||||        |
Db 61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114

Qy 121 VSS 123
        |||
Db 115 VSS 117
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RESULT 11
US-08-646-265A-99
; Sequence 99, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
;   APPLICANT: OHTOMO, Toshihiko
;   APPLICANT: SATO, Koh
;   APPLICANT: TSUCHIYA, Masayuki
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
;   NUMBER OF SEQUENCES: 132
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,265A
;   FILING DATE: 09-SEP-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP94/01763
;   FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 5-291078
;   FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
; INFORMATION FOR SEQ ID NO: 99:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 136 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-646-265A-99

Query Match   79.8%;   Score 523;   DB 4;   Length 136;
Best Local Similarity   83.7%;   Pred. No. 2.5e-45;
Matches 103;   Conservative   4;   Mismatches 10;   Indels 6;   Gaps 2;

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Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||:|||||||||||||||||||||||||||||||:|| ||||| |||
Db   20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||||:.:|||||||||||||||||:||||      |||||:|| |||||||
Db   80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN----QDYWGQGTTVT 133

Qy  121 VSS 123
          |||
Db  134 VSS 136
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RESULT 12
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
;   APPLICANT: OHTOMO, Toshihiko
;   APPLICANT: SATO, Koh
;   APPLICANT: TSUCHIYA, Masayuki
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
;   NUMBER OF SEQUENCES: 132
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,265A
;   FILING DATE: 09-SEP-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP94/01763
;   FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 5-291078
;   FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
; INFORMATION FOR SEQ ID NO: 109:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 269 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-646-265A-109

Query Match   79.8%;   Score 523;   DB 4;   Length 269;
Best Local Similarity   83.7%;   Pred. No. 5.7e-45;
Matches 103;   Conservative   4;   Mismatches 10;   Indels 6;   Gaps 2;

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Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db   23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||||:.:|||||||||||||||||:||||      |||||:|| |||||||
Db   83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN----QDYWGQGTTVT 136

Qy  121 VSS 123
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Db  137 VSS 139
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RESULT 13
US-08-561-521-13
; Sequence 13, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:

```
       ADDRESSEE: Townsend and Townsend Khourie and Crew
       STREET: One Market Plaza, Steuart Tower, Suite 2000
       CITY: San Francisco
       STATE: California
       COUNTRY: USA
       ZIP: 94105
  COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/08/561,521
       FILING DATE:
       CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
       APPLICATION NUMBER: US/08/186,269A
       FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
       NAME: Smith, William L.
       REGISTRATION NUMBER: 30,223
       REFERENCE/DOCKET NUMBER: 15270-14
  TELECOMMUNICATION INFORMATION:
       TELEPHONE: 415-543-9600
       TELEFAX: 415-543-5043
  INFORMATION FOR SEQ ID NO: 13:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 119 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: protein
  US-08-561-521-13

  Query Match       78.6%;  Score 515;  DB 2;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 1.4e-44;
  Matches  102;  Conservative   5;  Mismatches  12;  Indels   4;  Gaps   1;

  Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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  Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

  Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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  Db   61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS---GSNYWGQGTLVT 116

  Qy  121 VSS 123
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  Db  117 VSS 119

  RESULT 14
  PCT-US95-01219-13
  ; Sequence 13, Application PC/TUS9501219
  GENERAL INFORMATION:
       APPLICANT: Bendig, Mary M.
       APPLICANT: Leger, Olivier J.
       APPLICANT: Saldanha, Jose
       APPLICANT: Jones, S. Tarran
       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
       TITLE OF INVENTION: Adhesion Molecule VLA-4
       NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
       ADDRESSEE: Townsend and Townsend Khourie and Crew
       STREET: One Market Plaza, Steuart Tower, Suite 2000
       CITY: San Francisco
       STATE: California
       COUNTRY: USA
       ZIP: 94105
  COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
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       SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
       APPLICATION NUMBER: PCT/US95/01219
       FILING DATE: 25-JAN-1995
       CLASSIFICATION:
  PRIOR APPLICATION DATA:
       APPLICATION NUMBER: US 08/186,269
       FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
       NAME: Smith, William L.
       REGISTRATION NUMBER: 30,223
       REFERENCE/DOCKET NUMBER: 15270-14
  TELECOMMUNICATION INFORMATION:
       TELEPHONE: 415-543-9600
       TELEFAX: 415-543-5043
  INFORMATION FOR SEQ ID NO: 13:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 119 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: protein
  PCT-US95-01219-13

  Query Match       78.6%;  Score 515;  DB 5;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 1.4e-44;
  Matches  102;  Conservative   5;  Mismatches  12;  Indels   4;  Gaps   1;

  Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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  Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

  Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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  Db   61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS---GSNYWGQGTLVT 116

  Qy  121 VSS 123
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  Db  117 VSS 119

  RESULT 15
  US-08-561-521-12
  ; Sequence 12, Application US/08561521
  ; Patent No. 5840299
  GENERAL INFORMATION:
       APPLICANT: Bendig, Mary M.
       APPLICANT: Leger, Olivier J.
       APPLICANT: Saldanha, Jose
       APPLICANT: Jones, S. Tarran
       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
       TITLE OF INVENTION: Adhesion Molecule VLA-4
       NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
       ADDRESSEE: Townsend and Townsend Khourie and Crew
       STREET: One Market Plaza, Steuart Tower, Suite 2000
       CITY: San Francisco
       STATE: California
       COUNTRY: USA
       ZIP: 94105
  COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/08/561,521
       FILING DATE:
       CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
       APPLICATION NUMBER: US/08/186,269A
       FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
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;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX:   415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 119 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-12

Query Match         78.2%;  Score 512;  DB 2;  Length 119;
Best Local Similarity   82.9%;  Pred. No. 2.7e-44;
Matches  102;  Conservative   4;  Mismatches  13;  Indels   4;  Gaps   1;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            ||:||||||||||||||||||||||    :|||||||| |||||||:||||| :| |||
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy    121 VSS 123
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Db    117 VSS 119

Search completed: January  6, 2003, 13:19:10
Job time : 11.1879 secs
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            GenCore version 5.1.3
        Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:   January  6, 2003, 13:17:36 ; Search time 5.96364 Seconds
                                       (without alignments)
                                       390.875 Million cell updates/sec

Title:          US-09-155-739-11
Perfect score:  655
Sequence:       1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters:    117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
        1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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        3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
        4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
        5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
        6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
        7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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        9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
       10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
       11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
       12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
       13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
       14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	492	75.1	117	10	US-09-158-120A-17	Sequence 17, Appl
2	485.5	74.1	120	12	US-10-025-687-2	Sequence 2, Appli
3	484	73.9	180	10	US-09-748-960-6	Sequence 6, Appli
4	473	72.2	123	10	US-09-753-436-53	Sequence 53, Appl
5	472	72.1	123	10	US-09-753-436-86	Sequence 86, Appl
6	469	71.6	129	9	US-09-956-206A-77	Sequence 77, Appl
7	469	71.6	470	10	US-09-859-053-28	Sequence 28, Appl
8	459.5	70.2	120	12	US-10-025-687-1	Sequence 1, Appli
9	457	69.8	448	10	US-09-917-410-6	Sequence 6, Appli
10	456	69.6	249	1	US-08-779-457-48	Sequence 48, Appl
11	451.5	68.9	139	10	US-09-760-723-8	Sequence 8, Appli
12	451.5	68.9	139	10	US-09-355-925-8	Sequence 8, Appli
13	448.5	68.5	139	10	US-09-760-723-7	Sequence 7, Appli
14	448.5	68.5	139	10	US-09-355-925-7	Sequence 7, Appli
15	447.5	68.3	118	10	US-09-949-559-13	Sequence 13, Appl
16	447.5	68.3	132	10	US-09-811-737-10	Sequence 10, Appl
17	447.5	68.3	260	10	US-09-811-737-16	Sequence 16, Appl
18	446.5	68.2	120	10	US-09-971-543-11	Sequence 11, Appl
19	446.5	68.2	252	10	US-09-971-543-1	Sequence 1, Appli
20	442	67.5	119	10	US-09-905-243-79	Sequence 79, Appl
21	439	67.0	627	9	US-10-047-542-47	Sequence 47, Appl
22	437.5	66.8	270	10	US-09-976-118-2	Sequence 2, Appli
23	436.5	66.6	132	10	US-09-811-737-9	Sequence 9, Appli
24	436.5	66.6	260	10	US-09-811-737-17	Sequence 17, Appl
25	432	66.0	245	9	US-09-991-470-27	Sequence 27, Appl
26	431	65.8	117	9	US-09-956-206A-78	Sequence 78, Appl
27	431	65.8	136	9	US-09-956-206A-63	Sequence 63, Appl
28	429	65.5	117	10	US-09-158-120A-18	Sequence 18, Appl
29	428.5	65.4	135	9	US-09-249-011A-6	Sequence 6, Appli
30	428.5	65.4	461	9	US-09-249-011A-24	Sequence 24, Appl
31	428.5	65.4	515	10	US-09-825-012-66	Sequence 66, Appl
32	428.5	65.4	517	10	US-09-825-012-38	Sequence 38, Appl
33	428.5	65.4	519	10	US-09-825-012-76	Sequence 76, Appl
34	428.5	65.4	519	10	US-09-825-012-80	Sequence 80, Appl
35	428.5	65.4	521	10	US-09-825-012-71	Sequence 71, Appl
36	428.5	65.4	525	10	US-09-825-012-85	Sequence 85, Appl
37	428.5	65.4	527	10	US-09-825-012-43	Sequence 43, Appl
38	428.5	65.4	529	10	US-09-825-012-95	Sequence 95, Appl
39	428.5	65.4	531	10	US-09-825-012-90	Sequence 90, Appl
40	428.5	65.4	729	10	US-09-825-012-52	Sequence 52, Appl
41	428.5	65.4	730	10	US-09-825-012-49	Sequence 49, Appl
42	428.5	65.4	731	10	US-09-825-012-46	Sequence 46, Appl
43	428.5	65.4	739	10	US-09-825-012-61	Sequence 61, Appl
44	428.5	65.4	740	10	US-09-825-012-58	Sequence 58, Appl
45	428.5	65.4	741	10	US-09-825-012-55	Sequence 55, Appl

ALIGNMENTS

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RESULT 1
US-09-158-120A-17
; Sequence 17, Application US/09158120A
; Patent No. US2002010 2257A1
; GENERAL INFORMATION:
;   APPLICANT: JOHNSON, L.
;   TITLE OF INVENTION:  Human Murine Chimeric Antibodies Against
;   TITLE OF INVENTION:  Respiratory Syncytical Virus
;   NUMBER OF SEQUENCES: 49
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;     ADDRESSEE: STEWART & OLSTEIN
;     STREET:  6 BECKER FARM ROAD
;     CITY: ROSELAND
;     STATE: NEW JERSEY
;     COUNTRY: USA
;     ZIP: 07068
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 INCH DISKETTE
;     COMPUTER: P160
;     OPERATING SYSTEM: Windows95
;     SOFTWARE: MS Word 97
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/158,120A
;     FILING DATE: September 21, 1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/290,592
;     FILING DATE: August 15, 1994
;     APPLICATION NUMBER: 07/813,372
;     FILING DATE: December 23, 1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Olstein, Elliot M.
;     REGISTRATION NUMBER: 24,025
;     REFERENCE/DOCKET NUMBER: 469201-367
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 973-994-1700
;     TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 117 AMINO ACIDS
;     TYPE: AMINO ACID
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;        TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-158-120A-17

Query Match       75.1%;  Score 492;  DB 10;  Length 117;
Best Local Similarity  78.0%;  Pred. No. 2.5e-33;
Matches  96;  Conservative  7;  Mismatches  14;  Indels  6;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIYWVRQAPGQLEWIGWIDPENGNTVF 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
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Db   61 DPKFQGQVTMTRDTSTSTVYMELSSLRSEDTAVYYCA------YYGTSSFDFWGQGTLT 114

Qy  121 VSS 123
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Db  115 VSS 117

RESULT 2
US-10-025-687-2
; Sequence 2, Application US/10025687
; Patent No. US2002014255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-2

Query Match       74.1%;  Score 485.5;  DB 12;  Length 120;
Best Local Similarity  78.0%;  Pred. No. 8.4e-33;
Matches  96;  Conservative  7;  Mismatches  17;  Indels  3;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
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Qy  121 VSS 123
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Db  118 VSS 120

RESULT 3
US-09-748-960-6
; Sequence 6, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855.2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy
; OTHER INFORMATION: chain signal peptide
; NAME/KEY: SITE
; LOCATION: (19)...(20)
; OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-6

Query Match       73.9%;  Score 484;  DB 10;  Length 180;
Best Local Similarity  76.4%;  Pred. No. 1.6e-32;
Matches  94;  Conservative  9;  Mismatches  18;  Indels  2;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||||||||||||||||:  | ::||:|||||||:: ::: |
Db   20 QVQLVQSGAEVKKPGASVKVSCKGSGYTFTSYWMHWVRQAPGQRLEWIGEIDPSESNTNY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        ||||:|:|||:| ::||||||||||||||||||| ||| |:||:||||||
Db   80 NQKFKGRVTLTVDISASTAYMELSSLRSEDTAVYYCARGYDG--WDYAIDYWGQGTLVT 137

Qy  121 VSS 123
        |||
Db  138 VSS 140

RESULT 4
US-09-753-436-53
; Sequence 53, Application US/09753436
; Patent No. US2001002293A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,436
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-53

Query Match   72.2%; Score 473; DB 10; Length 123;
Best Local Similarity   78.0%; Pred. No. 8.7e-32;
Matches   96; Conservative   7; Mismatches   16; Indels   4; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db   5 QVQLVQSGAEVKKPGASVKVSCKASGYTFTDCIILWVRQAPGQGLEWMGKINPYFGTTTY 64

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db   65 NLKFKGRVTITADTSTSTAYMELSSLRSEDTAVYYCARKEAYPD----AMDYWGQGTLVT 120

Qy 121 VSS 123
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Db 121 VSS 123

RESULT 5
US-09-753-436-86
; Sequence 86, Application US/09753436
; Patent No. US20010029293A1
; GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRSPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-86

Query Match   72.1%; Score 472; DB 10; Length 123;
Best Local Similarity   77.2%; Pred. No. 1e-31;
Matches   95; Conservative   8; Mismatches   16; Indels   4; Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||:   :|||||||:||||:|:| |||| |:|
Db   5 QVQLVQSGAEVKKPGASVKVSCKASGYTFTVYMHWVRQAPGQGLEWMGYINPNTDYTEY 64

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          :|| :|||||||||:||||:|||||||||||||||| | || :|||||||||||
Db   65 NQRFQKRVTITADTSTSTAYMELSSLRSEDTAVYYCARWG--GN--SYGLDYWGQGTLVT 120

Qy 121 VSS 123
          |||
Db 121 VSS 123

RESULT 6
US-09-956-206A-77
; Sequence 77, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
           CERIANI, ROBERTO L.
           PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
       MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
       METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002

```
;          CLASSIFICATION: <Unknown>
;     PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 08/525,539
;          FILING DATE: 14-SEP-1995
;          APPLICATION NUMBER: PCT/US95/11683
;          FILING DATE: 14-SEP-1995
;          APPLICATION NUMBER: 08/487,598
;          FILING DATE: 7-JUNE-1995
;          APPLICATION NUMBER: 08/307,868
;          FILING DATE: 16-SEPT-1994
;     ATTORNEY/AGENT INFORMATION:
;          NAME: WITT, ERIC
;          REGISTRATION NUMBER: 44,408
;          REFERENCE/DOCKET NUMBER: 27633200 0101
;     TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (650) 813-5600
;          TELEFAX: (650) 494-0792
;          TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
;     SEQUENCE CHARACTERISTICS:
;          LENGTH: 129 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-956-206A-77

Query Match             71.6%;  Score 469;  DB 9;  Length 129;
Best Local Similarity   76.0%;  Pred. No. 1.9e-31;
Matches   98;  Conservative    3;  Mismatches   22;  Indels    6;  Gaps    2;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDP-ANGYTK 59
              |||||||||||||||||||||||||||   ||||||| ||||| :|   |:|
Db          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60

Qy         60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGN----YGVYAMDYWG 114
              | ||||||||||||| |||||||||||||||||||||     |    :|  ||||
Db         61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARAPGYGSGGGCYRGDYXFDYWG 120

Qy        115 QGTLVTVSS 123
              |||||||||
Db        121 QGTLVTVSS 129

RESULT 7
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US2002010 2658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Hori, No. US2002010 2658Aluaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match             71.6%;  Score 469;  DB 10;  Length 470;
Best Local Similarity   74.4%;  Pred. No. 6.7e-31;
Matches   93;  Conservative    8;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
              |||||||||||||||||||||||||||   |::|||||| ||||| |:  |:
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGTNY 79

Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
              |:| |||||| |::|||| |||||| ||||| ||||||||   | : | | : | |||||
Db         80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGYYHDAFDIWGQGTM 139

Qy        119 VTVSS 123
              |||||
Db        140 VTVSS 144

RESULT 8
US-10-025-687-1
; Sequence 1, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-1

Query Match             70.2%;  Score 459.5;  DB 12;  Length 120;
Best Local Similarity   77.2%;  Pred. No. 1e-30;
Matches   95;  Conservative    2;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
              ||||||||||||||| ||||||||||   ||:||||||| ||||| |:    |: |::|
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWQGGTLVT 120
              | |||||||||||: |||||||||||||||||||||||      :|  |||||||||||
Db         61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR--WGGDGFYAMDYWGQGTLVT 117

Qy        121 VSS 123
              |||
Db        118 VSS 120

RESULT 9
US-09-917-410-6
; Sequence 6, Application US/09917410
; Patent No. US2002009 8183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
;            CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
;                     MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
;                     PREVENTION OF ACUTE ORGAN DAMAGE AFTER
;                     EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Felfe & Lynch
;    STREET: 805 Third Avenue
;    CITY: New York
;    STATE: New York
;    COUNTRY: U.S.A.
;    ZIP: 10022
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: 3.5" Computer Disk
;    COMPUTER: IBM PC compatible
```

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       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: ASCII, WordPerfect 5.1
   CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/09/917,410
       FILING DATE: 26-Jul-2001
       CLASSIFICATION: <Unknown>
   PRIOR APPLICATION DATA:
       APPLICATION NUMBER: 08/578,953
       FILING DATE: <Unknown>
       APPLICATION NUMBER: EP 95 114 969.9
       FILING DATE: 19-Sep-95
   ATTORNEY/AGENT INFORMATION:
       NAME: Hanson, No. US20020098183Alman D.
       REGISTRATION NUMBER: 30,946
       REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
   TELECOMMUNICATION INFORMATION:
       TELEPHONE: (212) 688-9200
       TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
       LENGTH: 448 amino acid residues
       TYPE: amino acid
       TOPOLOGY: linear
   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-917-410-6

Query Match     69.8%;  Score 457;  DB 10;  Length 448;
Best Local Similarity   75.6%;  Pred. No. 5.8e-30;
Matches  93;  Conservative   8;  Mismatches  20;  Indels  2;  Gaps  60

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
       | |||||||||||:||||||||        :||||||||| |||| ||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIGYIYPYNDGTKY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
       : ||||||:    | : |||||||||||||||||| |||| ||
Db  61 NEKFKGRVTITSDESTNTAYMELSSLRSEDTAVYYCARE-EYGNVRY-FDVWGQGTLVT 118

Qy 121 VSS 123
       |||
Db 119 VSS 121


RESULT 10
US-08-779-457-48
; Sequence 48, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
;    APPLICANT: Carter, Paul J.
;    APPLICANT: Chiang, Nancy Y.
;    APPLICANT: Kyung, Jin Kim
;    APPLICANT: Matthews, William
;    APPLICANT: Rodrigues, Maria L.
;    TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
;    NUMBER OF SEQUENCES: 51
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Genentech, Inc.
;    STREET: 460 Point San Bruno Blvd
;    CITY: South San Francisco
;    STATE: California
;    COUNTRY: USA
;    ZIP: 94080
;    COMPUTER READABLE FORM:
;    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/779,457
;    FILING DATE:
;    CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/667197
;    FILING DATE: 06/20/96
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/585005
;    FILING DATE: 01/08/96
;    ATTORNEY/AGENT INFORMATION:
;    NAME: Lee, Wendy M.
;    REGISTRATION NUMBER: 40,378
;    REFERENCE/DOCKET NUMBER: P0986P2
;    TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 415/225-1994
;    TELEFAX: 415/952-9881
;    TELEX: 910/371-7168
;    INFORMATION FOR SEQ ID NO: 48:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 249 amino acids
;    TYPE: Amino Acid
;    TOPOLOGY: Linear
US-08-779-457-48

Query Match     69.6%;  Score 456;  DB 1;  Length 249;
Best Local Similarity   70.9%;  Pred. No. 4e-30;
Matches  90;  Conservative  11;  Mismatches  22;  Indels  4;  Gaps  1;

Qy   1 QVQLVQSGAEVKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
       : |||||||||||||||||||||        :||||||||| |||| :|:|  :| |
Db   1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYG---NYGVYAMDYWGQG 116
       : ||||||:|     | |||||| |  |:|||||||| |   |    :| ||:: ||:|
Db  61 AQKFQGRVTMTRDTSIGTAYMELSRLSDDTAVYYCARDRYYGSSAYHRGSYMDVWGRG 120

Qy 117 TLVTVSS 123
       |||||||
Db 121 TLVTVSS 127


RESULT 11
US-09-760-723-8
; Sequence 8, Application US/09760723
; Patent No. US20020034507A1
; GENERAL INFORMATION:
;    APPLICANT: KOISHIHARA, YASUO
;    TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
;    FILE REFERENCE: 053466/0295
;    CURRENT APPLICATION NUMBER: US/09/760,723
;    CURRENT FILING DATE: 2001-05-29
;    PRIOR APPLICATION DATE: 09/367,833
;    PRIOR FILING DATE: 1998-08-25
;    PRIOR APPLICATION NUMBER: PCT/JP98/00831
;    PRIOR FILING DATE: 1998-02-27
;    NUMBER OF SEQ ID NOS: 8
;    SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;    LENGTH: 139
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
;    OTHER INFORMATION: of H chain V region version s of humanized
;    OTHER INFORMATION: anti-HM1.24 antibody
US-09-760-723-8

Query Match     68.9%;  Score 451.5;  DB 10;  Length 139;
Best Local Similarity   72.4%;  Pred. No. 5.2e-30;
Matches  92;  Conservative   6;  Mismatches  18;  Indels  11;  Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
       |||||||||||||||||||||||        :||||||||| |||| |::
Db  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA----REGYGNYGVYAMDYWGQG 116
       : |||||||||||  | ||||||||||||||||||||     |  |  :|||:: ||:|
Db  80 SQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY------FDVWGQG 132
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```
Qy | 117 TLVTVSS 123
   |     | |||||
Db | 133 TTVTVSS 139

RESULT 12
US-09-355-925-8
; Sequence 8, Application US/09355925
; Patent No. US20020037288A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence H chain V region version s of
; OTHER INFORMATION: anti-HM1.24 antibody
US-09-355-925-8

Query Match             68.9%;  Score 451.5;  DB 10;  Length 139;
Best Local Similarity   72.4%;  Pred. No. 5.2e-30;
Matches   92; Conservative   6; Mismatches  18; Indels  11; Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||||   :: |||||||| ||||| | :| :|
Db  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA---REGYYGNYGVYAMDYWGQG 116
         |:|||:||:|||  |||||||||||||||||||       || |||||
Db  80 SQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY------FDYWGQG 132

Qy 117 TLVTVSS 123
       | |||||
Db 133 TTVTVSS 139

RESULT 13
US-09-760-723-7
; Sequence 7, Application US/09760723
; Patent No. US20020034507A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
; FILE REFERENCE: 053466/0295
; CURRENT APPLICATION NUMBER: US/09/760,723
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/367,833
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: PCT/JP98/00831
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of H chain V region version r of humanized
```

```
; OTHER INFORMATION: anti-HM1.24 antibody
US-09-760-723-7

Query Match             68.5%;  Score 448.5;  DB 10;  Length 139;
Best Local Similarity   71.7%;  Pred. No. 9e-30;
Matches   91; Conservative   7; Mismatches  18; Indels  11; Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||||   :: |||||||| ||||| | :| :|
Db  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA---REGYYGNYGVYAMDYWGQG 116
         |:|||:||||| |||||||||||||||||||        |:| |||||
Db  80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY------FDYWGQG 132

Qy 117 TLVTVSS 123
       | |||||
Db 133 TTVTVSS 139

RESULT 14
US-09-355-925-7
; Sequence 7, Application US/09355925
; Patent No. US20020037288A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of H chain V region version r of
; OTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7

Query Match             68.5%;  Score 448.5;  DB 10;  Length 139;
Best Local Similarity   71.7%;  Pred. No. 9e-30;
Matches   91; Conservative   7; Mismatches  18; Indels  11; Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||||   :: |||||||| ||||| | :| :|
Db  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCA---REGYGNYGVYAMDYWGQG 116
         |:|||:|||:|| |||||||||||||||||||        | || |||||
Db  80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYY------FDYWGQG 132

Qy 117 TLVTVSS 123
       | |||||
Db 133 TTVTVSS 139

RESULT 15
US-09-949-559-13
; Sequence 13, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
```

```
;    APPLICANT:   Chapman, Andrew Paul
;    APPLICANT:   King, David John
;    TITLE OF INVENTION: Biological Products
;    FILE REFERENCE: Carp-0095
;    CURRENT APPLICATION NUMBER: US/09/949,559
;    CURRENT FILING DATE:  2001-12-20
;    PRIOR APPLICATION NUMBER: 0013810.7GB
;    PRIOR FILING DATE: 2000-06-06
;    PRIOR APPLICATION NUMBER: 09/875,221
;    PRIOR FILING DATE: 2001-06-06
;    NUMBER OF SEQ ID NOS: 130
;    SOFTWARE: PatentIn version 3.1
;    SEQ ID NO 13
;    LENGTH: 118
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: ghhTNF40.4  (Figure  10)
US-09-949-559-13

Query Match        68.3%;    Score 447.5;  DB 10;   Length 118;
Best Local Similarity   75.6%;   Pred. No. 9.3e-30;
Matches    93;   Conservative   4;   Mismatches   21;   Indels    5;   Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||||||||||||||||||:  | ::||||||| |||| |: |—| |
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYVFTDYGMNWVRQAPGQGLEWMGWINTYIGEPIY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        | ||||| | ||| |||||||||||||||||||||     |  |||||||||||||||||
Db   61 AQKFQGRVTFTLDTSTSTAYMELSSLRSEDTAVYYCAR-----GYRSYAMDYWGQGTLVT 115

Qy  121 VSS 123
        |||
Db  116 VSS 118


Search completed: January  6, 2003, 13:29:32
Job time : 6.96364 secs
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              GenCore version 5.1.3
         Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       January  6, 2003, 13:12:26 ; Search time 11.4303 Seconds
                                           (without alignments)
                                           1034.490 Million cell updates/sec

Title:        US-09-155-739-11
Perfect score: 655
Sequence:     1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:       283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_73:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                  SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	488.5	74.6	178	2	S29594	Ig gamma chain (WM
2	477	72.8	120	2	S03471	Ig heavy chain V-D
3	473.5	72.3	118	2	S36265	Ig heavy chain V r
4	468	71.5	123	2	D33548	Ig heavy chain V-1
5	467	71.3	142	2	A32483	Ig heavy chain V r
6	465	71.0	117	2	S17586	Ig heavy chain V r
7	459.5	70.2	122	2	S06823	Ig heavy chain V r
8	456.5	69.7	132	2	PH0954	Ig heavy chain V r
9	455	69.5	116	2	S24289	Ig gamma chain V r
10	455	69.5	221	2	S49220	Ig gamma-1 chain -
11	450	68.7	129	2	S46393	Ig heavy chain V r
12	449	68.5	115	2	S03482	Ig heavy chain V-D
13	447.5	68.3	135	2	S49530	anti-Sm antibody V
14	447	68.2	120	2	S03484	Ig heavy chain V-D
15	446.5	68.2	136	2	PH0960	Ig heavy chain V r
16	444	67.8	136	2	S04576	Ig heavy chain pre
17	443	67.6	119	2	PH0961	Ig heavy chain V r
18	441.5	67.4	268	2	A56446	Ig heavy chain V r
19	439.5	67.1	104	2	PH1665	Ig heavy chain V r
20	439.5	67.1	114	4	A47271	nitrophenyl phosph
21	439	67.0	133	2	C33548	Ig heavy chain V-1
22	439	67.0	627	2	S14683	Ig mu chain precur
23	438.5	66.9	114	2	PH1667	Ig heavy chain V r
24	438.5	66.9	114	2	PH1666	Ig heavy chain V r
25	437.5	66.8	137	2	S52445	Ig heavy chain V r
26	436.5	66.6	120	2	S31999	Ig heavy chain V r
27	435.5	66.5	120	2	PH0962	Ig heavy chain V r
28	435.5	66.5	128	2	PH0952	Ig heavy chain V r
29	433.5	66.2	126	2	B33548	Ig heavy chain V-1
30	433	66.1	127	2	PH0955	Ig heavy chain V r
31	433	66.1	135	2	PH0953	Ig heavy chain V r
32	431	65.8	126	2	I44151	Ig heavy chain V r
33	429.5	65.6	108	2	PH1012	Ig heavy chain V r
34	429	65.5	125	2	PH0957	Ig heavy chain V r
35	427.5	65.3	143	1	E1HUND	Ig heavy chain pre
36	427	65.2	125	2	S68170	Ig heavy chain V-1
37	427	65.2	129	2	A33548	Ig heavy chain V r
38	426	65.0	127	2	S34014	Ig heavy chain V r
39	425	64.9	129	2	S36260	Ig heavy chain V r
40	424.5	64.8	147	2	PH1561	Ig heavy chain V r
41	424.5	64.8	171	2	S23623	Ig heavy chain V r
42	421	64.3	246	2	S38950	Ig gamma chain - m
43	421	64.3	446	2	S40295	Ig gamma-2a chain
44	420.5	64.2	122	2	PH1426	Ig heavy chain V r
45	420	64.1	121	2	S20783	Ig heavy chain V r

```
                  ALIGNMENTS

RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
; R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match         74.6%;   Score 488.5;  DB 2;    Length 178;
Best Local Similarity 75.6%;  Pred. No. 1.2e-36;
Matches  93;  Conservative  11;  Mismatches  14;  Indels   5;  Gaps    2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ::|| ||||||: |||||||:|| ||||||||||||::|||:||| |  | |||||||||:|
Db   14 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANGYTEY 73

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||| ||||::|||:::||||::||||||||||||     ||| ||||||| ||
Db   74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG---GNY-AYGMDYWGQGTSVT 128

Qy  121 VSS 123
          |||
Db  129 VSS 131

RESULT 2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1133983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
```

A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.8%; Score 477; DB 2; Length 120;
Best Local Similarity 75.6%; Pred. No. 8.8e-36;
Matches   93; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ::||| ||||||||||||||||||:|| |||||||| |||||||||||||| ||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||| ||||||||||||||||||||||| |||||||||||||||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116

Qy 121 LVTVSS 123
          |||
Db 117 LVTVSS 119

RESULT 3
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PIDN:CAA7929.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.3%; Score 473.5; DB 2; Length 118;
Best Local Similarity 76.2%; Pred. No. 1.8e-35;
Matches   96; Conservative 6; Mismatches 13; Indels 11; Gaps 2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||||| |||||||||||||||:|:| |
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE--GYYGNYGVYAMDYWGQGT 117
          |||||||||||| |||||||||||||||||||||||||| :|||||||||||
Db   61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY------LDYWGQGT 112

Qy 118 LVTVSS 123
          |||||
Db 113 LVTVSS 118

RESULT 4
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   71.5%; Score 468; DB 2; Length 123;
Best Local Similarity 74.8%; Pred. No. 5.7e-35;
Matches   92; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :||||||||||||||||||||::|||:
Db   1 QVQLVQSGAEVKKPGASVKVSCKEASGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   61 AEKFQGRVTITRDTSINTAYMELSLRSDDTAVYYCARASYCGYDCYYFDYWGQGTLVT 120

Qy 121 VSS 123
          |||
Db 121 VSS 123

RESULT 5
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

Query Match   71.3%; Score 467; DB 2; Length 142;
Best Local Similarity 73.2%; Pred. No. 8.2e-35;
Matches   93; Conservative 8; Mismatches 22; Indels 4; Gaps 1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||:|::|||
Db   11 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPNSGNSTNY 70

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQG 116
          |||||||||||| ||||||||||||||||||||||||| :|||||||||
Db   71 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy 117 TLVTVSS 123
          |||
Db 131 TLVTVSS 137

RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
forms.
A;Reference number: S17586; MUID:92015240; PMID:1656053
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA

```
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      71.0%;   Score 465;   DB 2;   Length 117;
Best Local Similarity   72.6%;   Pred. No. 1e-34;
Matches   90;  Conservative  15;  Mismatches  11;  Indels  8;  Gaps  3;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
Db   61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy  120 TVSS 123
Db  114 TVSS 117

RESULT 7
S06823
Ig heavy chain V region (clone IIC) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match      70.2%;   Score 459.5;   DB 2;   Length 122;
Best Local Similarity   73.4%;   Pred. No. 3.3e-34;
Matches   91;  Conservative  13;  Mismatches  13;  Indels  3;  Gaps  3;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy   60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTSV 119
Db   61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL--RRDAMGVDYWGQGTSV 118

Qy  120 TVSS 123
Db  119 TVSS 122

RESULT 8
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-112 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

```
;C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

Query Match      69.7%;   Score 456.5;   DB 2;   Length 132;
Best Local Similarity   72.0%;   Pred. No. 6.6e-34;
Matches   95;  Conservative   1;  Mismatches  27;  Indels  9;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-------EGYGNYGVYAMD 111
Db   61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120

Qy  112 YWGQGTLVTVSS 123
Db  121 VWGQGTTVTVSS 132

RESULT 9
S24289
Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match      69.5%;   Score 455;   DB 2;   Length 116;
Best Local Similarity   71.5%;   Pred. No. 7.8e-34;
Matches   88;  Conservative  13;  Mismatches  14;  Indels  8;  Gaps  2;

Qy    2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
Db    1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy   62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYGNYGVYAMDYWGQGTLVT 120
Db   61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY------FDYWGQGTTLT 113

Qy  121 VSS 123
Db  114 VSS 116

RESULT 10
S49220
Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
A;Accession: S49220
```

A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

```
Query Match     69.5%;   Score 455;  DB 2;   Length 221;
Best Local Similarity   70.7%;   Pred. No. 1.5e-33;
Matches  87;   Conservative  12;   Mismatches  20;   Indels  4;   Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||:|:||||| ||||||:|| |||||||||||||||||||||||||||||| ||
Db    1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYIGNYGVYAMDYWGQGTLVT 120
          |||||||| :||||:||| ||||||||||||||||  | ||||||| :|
Db   61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116

Qy  121 VSS 123
          |||
Db  117 VSS 119
```

RESULT 11
S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1135146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match     68.7%;   Score 450;  DB 2;   Length 129;
Best Local Similarity   70.5%;   Pred. No. 2.4e-33;
Matches  91;   Conservative  10;   Mismatches  22;   Indels  6;   Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||| |||||||||||||||||:|:||| :|:| |
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
          |||:| |||||||||||:||||| ||||||||||||| |
Db   61 AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYDSSGYYSANYYMDVWG 120

Qy  115 QGTLVTVSS 123
          || ||||||
Db  121 KGTTVTVSS 129
```

RESULT 12
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 21-Jan-2000
C;Accession: S03482; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT

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hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
A;Accession: S07453
A;Status: preliminary
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match     68.5%;   Score 449;  DB 2;   Length 115;
Best Local Similarity   70.2%;   Pred. No. 2.7e-33;
Matches  85;   Conservative  12;   Mismatches  18;   Indels  6;   Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||:||||| ||||||:||||||||||||||||||::|::|||||| |:|::||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||| :||||:||| :||||||||||||||||  | :|
Db   61 DPKFQGKATTTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR-----DYWGQGTTLT 114

Qy  121 V 121
          |
Db  115 V 115
```

RESULT 13
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match     68.3%;   Score 447.5;  DB 2;   Length 135;
Best Local Similarity   72.8%;   Pred. No. 4.3e-33;
Matches  91;   Conservative   7;   Mismatches  16;   Indels  11;   Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||  :|:||:||||||||||||:|: :|:| |
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC-AREGYYGNYGVYAMDYWGQGTL 118
          ||||:| |||||||||||:|||||:||||||||||  || |
Db   80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARARTGY--------NTWGQGTL 130

Qy  119 VTVSS 123
          |||||
Db  131 VTVSS 135
```

RESULT 14
S03484

Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   68.2%; Score 447; DB 2; Length 120;
Best Local Similarity   71.5%; Pred. No. 4.2e-33;
Matches   88; Conservative   11; Mismatches   20; Indels   4; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        :||| |||| ||||||||||||:|||| ||||||:|||: | || :|||||||| :||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
        |||| |||||||||:|| :||||||:| | ||||:|| | : ||||||||||||
Db   61 GPKFQGXATTTADTSSSAAYIQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy 121 VSS 123
        |||
Db 117 VSS 119

RESULT 15
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3

Query Match   68.2%; Score 446.5; DB 2; Length 136;
Best Local Similarity   69.1%; Pred. No. 5.3e-33;
Matches   94; Conservative   1; Mismatches   28; Indels   13; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
        ||||||||||||||||::|||||||||||||||||||||| |||| |+ | |||||
Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-------------EGYGNYGV 107
        ||||||||| | ||||||||||||||||||||||||||| |||
Db   61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120

Qy 108 YAMDYWGQGTLVTVSS 123
        | ||||||| ||||
Db 121 YGMDVWGQGTTVTVSS 136

Search completed: January 6, 2003, 13:18:20
Job time : 12.4303 secs

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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      January  6, 2003, 12:48:25 ; Search time 6.21212 Seconds
                                (without alignments)
                               821.231 Million cell updates/sec

Title:        US-09-155-739-11
Perfect score: 655
Sequence:     1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match  0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    SwissProt_40:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	427.5	65.3	147	1	HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1	HV03_MOUSE	P01747 mus musculu
3	408.5	62.4	139	1	HV07_MOUSE	P01751 mus musculu
4	405	61.8	117	1	HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1	HV02_MOUSE	P01746 mus musculu
6	396	60.5	117	1	HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1	HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1	HV13_MOUSE	P01757 mus musculu
9	375.5	57.3	118	1	HV51_MOUSE	P06330 mus musculu
10	373	56.9	117	1	HV12_MOUSE	P01756 mus musculu
11	371.5	56.7	137	1	HV11_MOUSE	P01755 mus musculu
12	369	56.3	138	1	HV48_MOUSE	P03980 mus musculu
13	364.5	55.6	120	1	HV50_MOUSE	P06329 mus musculu
14	360	55.0	121	1	HV01_MOUSE	P01745 mus musculu
15	360	55.0	136	1	HV15_MOUSE	P01759 mus musculu
16	355	54.2	125	1	HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1	HV1H_HUMAN	P80421 homo sapien
18	349	53.3	117	1	HV09_MOUSE	P01753 mus musculu
19	344.5	52.6	114	1	HV04_MOUSE	P01741 mus musculu
20	338	51.6	117	1	HV04_MOUSE	P01748 mus musculu
21	336	51.3	117	1	HV06_MOUSE	P01750 mus musculu
22	333.5	50.9	136	1	HV10_MOUSE	P01783 mus musculu
23	333	50.8	117	1	HV10_MOUSE	P01754 mus musculu
24	330.5	50.5	124	1	HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1	HV14_MOUSE	P01758 mus musculu
26	329	50.2	117	1	HV49_MOUSE	P06328 mus musculu
27	326	49.8	117	1	HV52_MOUSE	P06327 mus musculu
28	326	49.8	123	1	HV24_MOUSE	P01793 mus musculu
29	325.5	49.7	119	1	HV37_MOUSE	P01807 mus musculu
30	325.5	49.7	124	1	HV1D_HUMAN	P01760 homo sapien
31	324.5	49.5	119	1	HV38_MOUSE	P01808 mus musculu
32	323.5	49.4	119	1	HV40_MOUSE	P01810 mus musculu
33	320.5	48.9	122	1	HV3G_HUMAN	P01768 homo sapien
34	319	48.7			HV42_MOUSE	P01812 mus musculu
35	318.5	48.6			HV3A_HUMAN	P01762 homo sapien
36	318	48.5			HV3J_HUMAN	P01771 homo sapien
37	317	48.4			HV19_MOUSE	P01788 mus musculu
38	315	48.1			HV18_MOUSE	P01787 mus musculu
39	314.5	48.0			HV21_MOUSE	P01790 mus musculu
40	314	47.9			HV05_MOUSE	P01749 mus musculu
41	313	47.8			HV25_MOUSE	P01794 mus musculu
42	313	47.8			HV01_RAT	P01805 rattus norv
43	312	47.6			HV39_MOUSE	P01809 mus musculu
44	312	47.6			HV22_MOUSE	P01791 mus musculu
45	311.5	47.6			HV3H_HUMAN	P01769 homo sapien

```
                              ALIGNMENTS

RESULT 1
HV1C_HUMAN
ID   HV1C_HUMAN     STANDARD;      PRT;    147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02026; EIHUND.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    147                IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES      20     20                PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21                T -> V (IN REF. 2).
FT   CONFLICT     53     54                IH -> HI (IN REF. 2).
FT   CONFLICT     67     68                VG -> GV (IN REF. 2).
FT   CONFLICT    125    125                MISSING (IN REF. 2).
FT   NON_TER     147    147
SQ   SEQUENCE  147 AA;  16491 MW;  948F9F72A5366C20 CRC64;

Query Match             65.3%;  Score 427.5;  DB 1;  Length 147;
Best Local Similarity   64.1%;  Pred. No. 3.2e-36;
Matches   82;  Conservative   16;  Mismatches   25;  Indels   5;  Gaps   1;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          : ::::::::::::::::::::: :::::: :::::::: :: ::: :: ::: : :: :::
Db     20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR----EGYYGNYGVYAMDYWGQ 115
          :: ::::: :::::::: :::::::::::::::::::::    :: :: :: : ::::: ::
```

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Db    80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139

Qy   116 GTLVTVSS 123
          || |||||
Db   140 GTTVTVSS 147

RESULT 2
HV03_MOUSE
ID   HV03_MOUSE   STANDARD;   PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER       120    120
SQ   SEQUENCE   120 AA;   13307 MW;   FF04E4A167B654AF CRC64;

Query Match             62.4%;
Best Local Similarity   63.1%;
                               Pred. No. 1.8e-34;
Matches   77;  Conservative   18;  Mismatches   25;  Indels   2;  Gaps   1;

Qy    2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
         |||:||||| ::| |:||:||||||:||||:|:|||||||
Db    1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWKVKQRPGQGLEWIGYINPGNGYTKYN 60
Qy   62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDVWGQGTLVTV 121
         ||:|:| | |:||||| || |||:|:| ||||||:|
Db   61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLFV 118

Qy  122 SS 123
         ||
Db  119 SS 120

RESULT 3
HV07_MOUSE
ID   HV07_MOUSE   STANDARD;   PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed.  Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     19
FT   CHAIN         20    139    IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN        20     49    FRAMEWORK-1.
FT   DOMAIN        50     54    COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        55     68    FRAMEWORK-2.
FT   DOMAIN        69     85    COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        86    117    FRAMEWORK-3.
FT   DOMAIN       118    124    D SEGMENT.
FT   DOMAIN       125    139    JH2 SEGMENT.
FT   DISULFID      41    115    BY SIMILARITY.
FT   NON_TER      139    139
SQ   SEQUENCE   139 AA;   15419 MW;   1B57DD4FD0C9F465 CRC64;

Query Match             62.4%;
Best Local Similarity   62.6%;
                               Pred. No. 2.4e-34;
Matches   77;  Conservative   18;  Mismatches   25;  Indels   3;  Gaps   1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         |||:|||||||:|||||:||:||||||:||||:|:|||||::|:|:|::|||||||:||
Db   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDVWGQGTLVT 120
         : :|||||||:||||||| |||:|:||||:|||||||| :||:|:
Db   80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT 136

Qy  121 VSS 123
         |||
Db  137 VSS 139

RESULT 4
HV1B_HUMAN
ID   HV1B_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8314028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
```

RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117
FT   NON_TER   117   117   IG HEAVY CHAIN V-I REGION HG3.
SQ   SEQUENCE   117 AA;   12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match   61.8%; Score 405; DB 1; Length 117;
Best Local Similarity   79.6%; Pred. No. 4.5e-34;
Matches   78; Conservative   5; Mismatches   15; Indels   0; Gaps   0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIIHWRQAPGQRLEWMGRIDPANGYTKY 60
            ||||||||||||||||||||||||||||||:||:|||||||||||||||||||||||||
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIIHWRQAPGQGLEWMGRIDPANGYTKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR   98
            ||||||| |:| |||||||||||||||||||||||||||
Db   80 AQKFQGRVTMRDTSTSTVYMELSSLRSEDTAVYYCAR   117

RESULT 5
HV02_MOUSE
ID   HV02_MOUSE   STANDARD;   PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   140   IG HEAVY CHAIN V REGION 93G7.
FT   NON_TER   140   140
SQ   SEQUENCE   140 AA;   15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match   60.9%; Score 399; DB 1; Length 140;
Best Local Similarity   61.0%; Pred. No. 2.2e-33;
Matches   75; Conservative   19; Mismatches   27; Indels   2; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            :|||||||:|||: :||||||||:|||||||| |:||| |||| ||||::|:|||::||
Db   20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGSYYGNYGVYAMDYWGQGTLVT 120
            :|||||| ::|| : ||||||:|||| ::||| ||| |:| ::| | | | ::|
Db   80 NEKFKGKTLTVDKSSSTAYMQLRSLTSEDSAVFYCARSHYG--GSYDFDYWGQGTPLT 137

Qy 121 VSS 123
            |||
Db 138 VSS 140

RESULT 6
HVIG_HUMAN
ID   HVIG_HUMAN   STANDARD;   PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117   IG HEAVY CHAIN V-I REGION V35.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA;   13009 MW; BE61CE63F8CE97BD CRC64;

Query Match   60.5%; Score 396; DB 1; Length 117;
Best Local Similarity   78.6%; Pred. No. 3.7e-33;
Matches   77; Conservative   5; Mismatches   16; Indels   0; Gaps   0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNY 79

```
Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
         |||||||| | ||| |||||| ||||||||||| |
Db   80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117

RESULT 7
HV1A_HUMAN
ID   HV1A_HUMAN     STANDARD;      PRT;    117 AA.
AC   P01742;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC       MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR   PIR; A02023; G1HUEU.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;   12472 MW;   99D60ADAEBD52818 CRC64;

Query Match             59.5%;  Score 390;  DB 1;  Length 117;
Best Local Similarity   68.3%;  Pred. No. 1.5e-32;
Matches   84;  Conservative    8;  Mismatches  25;  Indels    6;  Gaps    2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||| ||||||||||||  |||:|||||||||| | | |||
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         ||||||||||    ||::||||||||||||| |||:|:::      |
Db   61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114

Qy  121 VSS 123
         |||
Db  115 VSS 117

RESULT 8
HV13_MOUSE
ID   HV13_MOUSE     STANDARD;      PRT;    117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96              BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;   13024 MW;   292E2AF4BE447E41 CRC64;

Query Match             57.7%;  Score 378;  DB 1;  Length 117;
Best Local Similarity   58.5%;  Pred. No. 2.4e-31;
Matches   72;  Conservative   20;  Mismatches  25;  Indels    6;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         :||||||  || :|||||||||||||||  |:|:: :|:|||:|: :|||:| |||
Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         :||| ||| :|||:||:|||||::||||::|||||||  |
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----WYFDVWGAGTTVT 114

Qy  121 VSS 123
         |||
Db  115 VSS 117

RESULT 9
HV51_MOUSE
ID   HV51_MOUSE     STANDARD;      PRT;    118 AA.
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02040; MIMS38.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98              V SEGMENT.
FT   DOMAIN       99    104              D SEGMENT.
FT   DOMAIN      105    118              J SEGMENT.
FT   DISULFID     22     96
FT   NON_TER     118    118              BY SIMILARITY.
```

SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

```
Query Match
Best Local Similarity  57.3%;       Score 375.5;  DB 1;  Length 118;
                       58.5%;       Pred. No. 4.3e-31;
Matches  72;  Conservative  17;  Mismatches  29;  Indels  5;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
          :||| ||| |::|: :||||||:||||| |||: : || |:|  :|| | | ||
Db    1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY  60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
          : ||:|: : |||  |||||||:  || |||||||||||    :|| | || | || ||
Db   61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR----GYGYDPFDVWGTGTTVT 115

Qy  121 VSS 123
          |||
Db  116 VSS 118
```

RESULT 10
HV12_MOUSE
```
ID  HV12_MOUSE    STANDARD;    PRT;   117 AA.
AC  P01756;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Ig heavy chain V region MOPC 104E.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX  MEDLINE=83075344; PubMed=6816276;
RA  Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA  Hood L.E.;
RT  "Complete amino acid sequence of a mouse mu chain: homology among
RT  heavy chain constant region domains.";
RL  Biochemistry 21:5415-5424(1982).
CC  -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC      PROTEIN HAS ALSO BEEN DETERMINED.
CC  -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR  PIR; A02039; MHMS4E.
DR  HSSP; P01789; 1MCP.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
KW  Immunoglobulin V region; Glycoprotein.
FT  DISULFID      22     96       BY SIMILARITY.
FT  CARBOHYD      55     55       N-LINKED (GLCNAC. . .) (COMPLEX).
FT  NON_TER      117    117
SQ  SEQUENCE  117 AA;  12983 MW;  3CF8ACE4BE447E41 CRC64;
```

```
Query Match
Best Local Similarity  56.9%;       Score 373;  DB 1;  Length 117;
                       59.3%;       Pred. No. 7.6e-31;
Matches  73;  Conservative  19;  Mismatches  25;  Indels  6;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
          :||| ||| |::|: :||||||:||||| |||: : || |:|  :|| | | ||
Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY  60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
          : ||:|: : |||  ||||||::  || |||||||||||:    :|| | || | || ||
Db   61 NQKFKGKATLTVDKSSSATYMQLNSLTSEDSAVYYCARD----YDWY-FDVWGAGTTVT 114

Qy  121 VSS 123
          |||
Db  115 VSS 117
```

RESULT 11
HV11_MOUSE

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ID  HV11_MOUSE    STANDARD;    PRT;   137 AA.
AC  P01755;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region S43 precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81234548; PubMed=6788376;
RA  Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA  Baltimore D.;
RT  "Heavy chain variable region contribution to the NPb family of
RT  antibodies: somatic mutation evident in a gamma 2a variable region.";
RL  Cell 24:625-637(1981).
CC  -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC      MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC      (NPB ANTIBODIES).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
DR  EMBL; J00539; AAA38172.1; -.
DR  PIR; A02038; G2MS43.
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL         1     19
FT  CHAIN         20    137      IG HEAVY CHAIN V REGION S43.
FT  DOMAIN        20     49      FRAMEWORK-1.
FT  DOMAIN        50     54      COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN        55     68      FRAMEWORK-2.
FT  DOMAIN        69     85      COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN        86    117      FRAMEWORK-3.
FT  DOMAIN       118    122      D SEGMENT.
FT  DOMAIN       123    137      JH2 SEGMENT.
FT  DISULFID      41    115      BY SIMILARITY.
FT  NON_TER      137    137
SQ  SEQUENCE  137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;
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Query Match
Best Local Similarity  56.7%;       Score 371.5;  DB 1;  Length 137;
                       60.2%;       Pred. No. 1.3e-30;
Matches  74;  Conservative  14;  Mismatches  30;  Indels  5;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
          :||| |||:|| :||||||:|| ||||||:|::|:||:||:||:|||:|||:||:|
Db   20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY  79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
          : :: |:|:|:|  ||||| |:|::||:|::|||||||||:   :|| |  ::|| | ||
Db   80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134

Qy  121 VSS 123
          |||
Db  135 VSS 137
```

RESULT 12
HV48_MOUSE
```
ID  HV48_MOUSE    STANDARD;    PRT;   138 AA.
AC  P03980;
DT  23-OCT-1986 (Rel. 02, Created)
```

```
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      128    138       FRAMEWORK-4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;

Query Match             56.3%;  Score 369;  DB 1;  Length 138;
Best Local Similarity   58.1%;  Pred. No. 2.3e-30;
Matches   72;  Conservative   20;  Mismatches   26;  Indels    6;  Gaps

Qy      1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||| :|:||||||||||:|||||||||||:|||||||: :|||||||||||||| |
Db     20  QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79

Qy     61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV 119
           :.|:|||||:.|:||||:|||||:||:|||| ||||  :||    :  |   |||||||
Db     80  NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF----VYWGQGTLV 134

Qy    120  TVSS 123
           ||:|
Db    135  TFSA 138

RESULT 13
ID   HV50_MOUSE      STANDARD;      PRT;   120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MRMS15.
DR   HSSP; P01810; 2FBJ.
```

```
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98       V SEGMENT.
FT   DOMAIN       99    105       D SEGMENT.
FT   DOMAIN      106    120       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13311 MW;  914453F426F09834 CRC64;

Query Match             55.6%;  Score 364.5;  DB 1;  Length 120;
Best Local Similarity   56.1%;  Pred. No. 5.6e-30;
Matches   69;  Conservative   19;  Mismatches   32;  Indels    3;  Gaps    1;

Qy      1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY 60
           ||||:|: ||||||||||||||||||||||||||:||||||: :||||||||||||| |
Db      1  QVQLLQPGTELVKPGASVNLSCKASGYTFSYWMHWIRQPGQGLEWIGGINPSNGGTNY 60

Qy     61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           :.|:||||||:.|:||||:|||||||||:|||||||||||  : |: :  |  |||||||
Db     61  NEKFKSKATLTVDKSSSTAYMQLSTPTSEDSAVYYCARWDYEGD---RYFDVWGTGTTVT 117

Qy    121  VSS 123
           |||
Db    118  VSS 120

RESULT 14
ID   HV01_MOUSE      STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
DR   PIR; A02027; GVMS11.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;

Query Match             55.0%;  Score 360;  DB 1;  Length 121;
Best Local Similarity   55.3%;  Pred. No. 1.6e-29;
Matches   68;  Conservative   23;  Mismatches   30;  Indels    2;  Gaps    2;

Qy      1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY 60
           ||||:|:||||||||||||||||||||| :|||: :|||||||:||||||||||:: |:|
Db      1  EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy     61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
```

```
Db      61  NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT  118
            :: |:|||||::||||||||:|||| |||:|:|:||| |:|  |  ||||||:|

Qy     121  VSS 123
            |||
Db     119  VSS 121


RESULT 15
ID   HV15_MOUSE     STANDARD;      PRT;    136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region BCL1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long  as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;

Query Match             55.0%;  Score 360;  DB 1;  Length 136;
Best Local Similarity   56.9%;  Pred. No. 1.8e-29;
Matches    70;  Conservative   17;  Mismatches   30;  Indels    6;  Gaps    2;

Qy      1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
           ||||| ||  ||:: || ||  ||||:|| ::|:|||:|:: : |||:| : :|||| |
Db     20  QVQLQQSGPEVVRPGVSVKISCKSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY  79

Qy     61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
           | :|:|: :|:|: || || :|  | ||| ||||| ||||      |||||| ||||| :|
Db     80  NQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--YYGNY---FDYWGQGTTLT  133

Qy    121  VSS  123
           |||
Db    134  VSS  136


Search completed: January  6, 2003, 13:15:47
Job time : 6.21212 secs
```

```
                    GenCore version 5.1.3
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      January 6, 2003, 13:10:51 ; Search time 23.1091 Seconds
                                         (without alignments)
                                         1096.702 Million cell updates/sec

Title:          US-09-155-739-11
Perfect score:  655
Sequence:       1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:        671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SPTREMBL_21:*
           1:   sp_archea:*
           2:   sp_bacteria:*
           3:   sp_fungi:*
           4:   sp_human:*
           5:   sp_invertebrate:*
           6:   sp_mammal:*
           7:   sp_mhc:*
           8:   sp_organelle:*
           9:   sp_phage:*
          10:   sp_plant:*
          11:   sp_rodent:*
          12:   sp_virus:*
          13:   sp_vertebrate:*
          14:   sp_unclassified:*
          15:   sp_rvirus:*
          16:   sp_bacteriap:*
          17:   sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	457.5	69.8	124	4	Q9UL92	Q9UL92 homo sapien
2	440.5	67.3	159	4	Q96QS0	Q96QS0 homo sapien
3	440	67.2	468	11	Q99L31	Q99131 mus musculu
4	432	66.0	109	11	Q9JL85	Q99JL85 mus musculu
5	432	66.0	119	4	Q9UL94	Q9UL94 homo sapien
6	432	66.0	614	4	Q96GA6	Q96GA6 homo sapien
7	428	65.3	119	5	Q9GYZ2	Q9GYZ2 schistosoma
8	428	65.3	125	4	Q9UL95	Q9UL95 homo sapien
9	427	65.2	146	11	Q924Q3	Q924Q3 mus musculu
10	422	64.4	473	11	Q9D8L4	Q9D8L4 mus musculu
11	422	63.4	145	11	Q924R4	Q924R4 mus musculu
12	415.5	63.4	145	11	Q924R1	Q924R1 mus musculu
13	412	62.9	146	11	Q924R8	Q924R8 mus musculu
14	411.5	62.8	116	4	Q9UL89	Q9UL89 homo sapien
15	409.5	62.5	145	11	Q924Q6	Q924Q6 mus musculu
16	408.5	62.4	145	11	Q924Q7	Q924Q7 mus musculu
17	408.5	62.4	473	11	Q99L25	Q99125 mus musculu
18	408	62.3	142	11	Q924Q1	Q924q1 mus musculu
19	407.5	62.2	143	11	Q924P9	Q924p9 mus musculu
20	407	62.1	117	11	Q9QXE9	Q9qxe9 mus musculu
21	405.5	61.9	145	11	Q924Q9	Q924q9 mus musculu
22	405	61.8	140	11	Q924R2	Q924r2 mus musculu
23	403.5	61.6	143	11	Q924R0	Q924r0 mus musculu
24	403.5	61.6	145	11	Q924P7	Q924p7 mus musculu
25	399	60.9	142	11	Q924Q2	Q924q2 mus musculu
26	399	60.9	150	4	Q9Y298	Q9y298 homo sapien
27	398.5	60.8	500	4	Q9BRV0	Q9brv0 homo sapien
28	398	60.8	481	11	Q91WT1	Q91wt1 mus musculu
29	394.5	60.2	143	11	Q924R7	Q924r7 mus musculu
30	393.5	60.1	145	11	Q924R3	Q924r3 mus musculu
31	391.5	59.8	488	11	Q91WR1	Q91wr1 mus musculu
32	389.5	59.5	137	11	Q924R6	Q924r6 mus musculu
33	389.5	59.5	143	11	Q91VA2	Q91va2 mus musculu
34	388.5	59.3	139	11	Q924R5	Q924r5 mus musculu
35	388.5	59.3	141	11	Q924Q4	Q924q4 mus musculu
36	386	59.0	118	11	Q921C4	Q921c4 mus musculu
37	386	59.0	117	11	Q9QXF0	Q9qxf0 mus musculu
38	384	58.6	157	4	O95978	O95978 homo sapien
39	383.5	58.5	613	11	Q8VCX7	Q8vcx7 mus musculu
40	381.5	58.2	143	11	Q91V67	Q91v67 mus musculu
41	381.5	58.2	463	11	Q99LC4	Q99LC4 mus musculu
42	381	58.2	146	11	Q924Q8	Q924q8 mus musculu
43	380.5	58.1	143	11	Q924Q5	Q924q5 mus musculu
44	380	58.0	144	11	Q924P5	Q924p5 mus musculu
45	380	58.0	484	11	Q99LA6	Q99la6 mus musculu

ALIGNMENTS

```
RESULT 1
Q9UL92
ID   Q9UL92          PRELIMINARY;     PRT;    124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;   13580 MW;  1BAAACBD96ACD2A2 CRC64;

Query Match             69.8%;  Score 457.5;  DB 4;  Length 124;
Best Local Similarity   69.5%;  Pred. No. 2.8e-40;  -.
Matches   91;  Conservative    9;  Mismatches  16;  Indels  15;  Gaps  2;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||:|||||||||||||||||||||||||  :|||||||||||| |||::|:| | |
Db      1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
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Qy   61 DPKFQGRVTITADTSASTAYMELSLRSEDTAVYYCAREGYYGNYGVYAM--------DY 112
        ||||||:: ||| ||  ||||||||||||||||       |:| :       ||
Db   61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR------GLYVVVPAAFSRFDY 113

Qy  113 WGQGTLVTVSS 123
        |||||||||||
Db  114 WGQGTLVTVSS 124

RESULT 2
Q96QS0
ID   Q96QS0         PRELIMINARY;        PRT;    159 AA.
AC   Q96QS0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative matrix cell adhesion molecule-3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tilson M.D.;
RT   "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT   mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY039025; AAK82649.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
SQ   SEQUENCE 159 AA;  17497 MW;  5D29537E881FAF02 CRC64;

Query Match         67.3%;   Score 440.5;  DB 4;  Length 159;
Best Local Similarity   64.9%;   Pred. No. 2.3e-38;
Matches   87;  Conservative  13;  Mismatches  19;  Indels  15;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||||||||||||||||||||::  : |:|||||||||:|||||||||||||||
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSLRSEDTAVYYCARE---------GYYGNYGVYA 109
        ||||:: : |||||||||||||||||||||||||||||         ||  |
Db   80 SQKFQGRLIMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFY----YYG 135

Qy  110 MDYWGQGTLVTVSS 123
        ||:||||| |||||
Db  136 MDVWGQGTTVTVSS 149

RESULT 3
Q99L31
ID   Q99L31         PRELIMINARY;        PRT;    468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
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DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1, 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 468 AA;  51661 MW;  96352328B3332ADB CRC64;

Query Match         67.2%;   Score 440;  DB 11;  Length 468;
Best Local Similarity   67.5%;   Pred. No. 1e-37;
Matches   83;  Conservative  16;  Mismatches  20;  Indels  4;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        :||||||| :|||||||||||||||||::  :|||| -:| :|||||||||| : |||
Db   20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        |||  : |:||||||||||||||:|:||||||||:||||| || ||   :|   ||| :|
Db   80 APKFQDKATITADTSSNTAYLQLSSLTSEDTATYYCARNLLYGGY----YDYWGQGTTIT 135

Qy  121 VSS 123
        ||
Db  136 VSS 138

RESULT 4
Q9JL85
ID   Q9JL85         PRELIMINARY;        PRT;    109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206021; AAF69319.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      109    109
SQ   SEQUENCE 109 AA;  11944 MW;  DFE615FE6CED4EDE CRC64;

Query Match         66.0%;   Score 432;  DB 11;  Length 109;
Best Local Similarity   68.7%;   Pred. No. 1.1e-37;
Matches   79;  Conservative  15;  Mismatches  15;  Indels  6;  Gaps  1;

Qy    9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
        :|| |||||||||||||||||||||||||||||||||||||||||| :::|||||||||
Db    1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy   69 TITADTSASTAYMELSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
        |||:||||:||||||||||||||||||      |||||| :|   ||||| :|||
Db   61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR------GAVFDYWGQGTALTVSS 109

RESULT 5
Q9UL94
ID   Q9UL94         PRELIMINARY;        PRT;    119 AA.
AC   Q9UL94;
```

DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   MEDLINE=9827139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035020; AAD56256.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   119   119
SQ   SEQUENCE   119 AA;   13205 MW;   13E64F5345F4A16E CRC64;

Query Match   66.0%; Score 432; DB 4; Length 119;
Best Local Similarity   70.7%; Pred. No. 1.3e-37;
Matches   87; Conservative   10; Mismatches   22; Indels   4; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||:|||||||||||||||||||| :||||||||| |||||:|||||||||:|||:|
Db   1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||:||:| ||| |||||||||||||||||||| : | : FDPWGQGTLVT
Db   61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116

Qy 121 VSS 123
          |||
Db 117 VSS 119

RESULT 6
Q96GA6
ID   Q96GA6   PRELIMINARY;   PRT;   614 AA.
AC   Q96GA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:15420).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009851; AAH09851.1; -.
DR   InterPro; IPR000005; HTHAraC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   614 AA;   67921 MW;   55EF536E77AA9BBB CRC64;

Query Match   66.0%; Score 432; DB 4; Length 614;

Best Local Similarity   71.5%;   Pred. No. 9.9e-37;
Matches   88; Conservative   9; Mismatches   24; Indels   2; Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||:|||||||| ||:|||||||||| :||||||||| |||||:|||||||||:|||:|
Db   20 QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||| | ||:||| ||||||||||||:||||||||| : : | |:
Db   80 AQKFQDRVTITRDSRSMNTAYMELSSLRSEDTAMYYCAR-GYSSSWD-DAFDIWGQGTMVT 137

Qy 121 VSS 123
          |||
Db 138 VSS 140

RESULT 7
Q9GYZ2
ID   Q9GYZ2   PRELIMINARY;   PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE   (Fragment).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01573; SUPERTUBBY.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER   1   1
FT   NON_TER   119   119
SQ   SEQUENCE   119 AA;   13567 MW;   BA93873FD5FA6AB CRC64;

Query Match   65.3%;   Score 428; DB 5;   Length 119;
Best Local Similarity   66.7%;   Pred. No. 3.3e-37;
Matches   82; Conservative   17; Mismatches   20; Indels   4; Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||| :||||||||| :|:|:||||||:|||: :|:|
Db   1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYIMNWVRQAPGHGLEWIGYINPSRGYTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          :||::| | | ||| | ||||| :|:| ||||||| : | :|YYDDH YCLDYWGQGTTVT
Db   61 NQKFKDRVTMTDKSFSTAYMDLRSLRSADSAVYYCAR--YYDDH--YCLDYWGQGTTVT 116

Qy 121 VSS 123
          |||
Db 117 VSS 119

RESULT 8
Q9UL95
ID   Q9UL95   PRELIMINARY;   PRT;   125 AA.
AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)

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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035019; AAD56255.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C23288EAC CRC64;

Query Match             65.3%;  Score 428;  DB 4;  Length 125;
Best Local Similarity   68.8%;  Pred. No. 3.5e-37;
Matches   86;  Conservative  10;  Mismatches  27;  Indels  2;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :||:|||||||||||||||||| |:|||||||||| ||||||||||||||||:|:| | |
Db    1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
          | |||||||||:||:|| ||:||||||||| |||||||||          ||| |||||
Db   61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGRIAAAGDAFDIWGQGTM 120

Qy  119 VTVSS 123
          |:|||
Db  121 VTVSS 125


RESULT 9
ID   Q92AQ3
Q92AQ3   Q92AQ3;
AC   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067797; BAB63282.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER      1      1
FT   NON_TER    146    146
SQ   SEQUENCE   146 AA;  16136 MW;  C8A8DD6E1955807F CRC64;

Query Match             65.2%;  Score 427;  DB 11;  Length 146;
Best Local Similarity   65.9%;  Pred. No. 5.5e-37;
Matches   81;  Conservative  17;  Mismatches  23;  Indels  2;  Gaps  1;
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Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||| |||||||||||||||||||||||||||:||||||||||:.||||||||||| | |
Db    1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTSLVT 120
          : | :|: : :|| : ||||||||||||||||||:||||| :|| :|||||||| ||||
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSLY--DYGDYAMDYWGQGTSVT 118

Qy  121 VSS 123
          |||
Db  119 VSS 121


RESULT 10
Q9D8L4
ID   Q9D8L4      PRELIMINARY;      PRT;    473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009Rik protein.
GN   IGH-1 OR 1810060009RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig-1.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

Query Match             64.48%;  Score 422;  DB 11;   Length 473;
Best Local Similarity   65.9%;  Pred. No. 8e-36;
Matches   81;  Conservative  19;  Mismatches  19;  Indels  4;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||| ||||| ||||||||:|||:|||||| ||||:|| :| | :|:| | || :| | |
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Db   20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYIINWVKQRPGQGLEWIGKIGPSGSGSTYY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Db   80 NEKFFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY--DYDWFA--YWGQGTLVT 135

Qy 121 VSS 123

Db 136 VSA 138

RESULT 11
Q924R4
ID   Q924R4;   PRELIMINARY;   PRT;   145 AA.
AC   Q924R4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067785; BAB63270.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA; 16081 MW; ECDB1A135E05B8AA CRC64;

Query Match   63.4%; Score 415.5; DB 11; Length 145;
Best Local Similarity   65.0%; Pred. No. 8.7e-36;
Matches   80; Conservative 17; Mismatches 23; Indels   3; Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDY--DYD-YAMDYWGQGTSVT 117

Qy 121 VSS 123

Db 118 VSS 120

RESULT 12
Q924R1
ID   Q924R1;   PRELIMINARY;   PRT;   145 AA.
AC   Q924R1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-

RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067789; BAB63274.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match   63.4%; Score 415.5; DB 11; Length 145;
Best Local Similarity   64.2%; Pred. No. 8.7e-36;
Matches   79; Conservative 16; Mismatches 25; Indels   3; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR---YDGSSFYAMDYWGQGTSVT 117

Qy 121 VSS 123

Db 118 VSS 120

RESULT 13
Q924R8
ID   Q924R8;   PRELIMINARY;   PRT;   146 AA.
AC   Q924R8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067781; BAB63266.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1   1
FT   NON_TER   146   146
SQ   SEQUENCE   146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match   62.9%; Score 412; DB 11; Length 146;
Best Local Similarity   63.4%; Pred. No. 2e-35;
Matches   78; Conservative 19; Mismatches 24; Indels   2; Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR-SYYGS-SLYYFDYWGQGTTLT 118

Qy 121 VSS 123

Db 119 VSS 121

RESULT 14
Q9UL89
ID   Q9UL89   PRELIMINARY;   PRT;   116 AA.

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AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035025; AAD56261.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM004406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     116     116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;

Query Match             62.8%;  Score 411.5;  DB 4;  Length 116;
Best Local Similarity   72.5%;  Pred. No. 1.7e-35;
Matches   87;  Conservative    3;  Mismatches   25;  Indels    5;  Gaps    2;

Qy      5  VQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKF  64
           ||||||||||||::||||||||  ||||||||||||||| |||||||| | |- || -|
Db      1  VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF  60

Qy     65  QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS  123
           ||||||||| :||||||||||||||||||||||       :| |  || |||||||||||
Db     61  QGRVTITADKSTSTAYMELSSLRSEDTAVYYCAS----SNWGPYWYFDLWGRGTLVTVSS  116
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RESULT 15
Q924Q6
ID   Q924Q6         PRELIMINARY;      PRT;   145 AA.
AC   Q924Q6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067794; BAB63279.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1       1
FT   NON_TER     145     145
SQ   SEQUENCE   145 AA;  16011 MW;  9BC0846D40DF97EA CRC64;

Query Match             62.5%;  Score 409.5;  DB 11;  Length 145;
Best Local Similarity   63.2%;  Pred. No. 3.7e-35;
Matches   79;  Conservative   17;  Mismatches   22;  Indels    7;  Gaps    2;

Qy      1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
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```
Db      1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  60
           |||| | |||: |||| |||||:::|||||||||||||||:: |||||||::| |||
Qy     61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE--GYYGNYGVYAMDYWGQGTL  118
           : |: :|:| | :||||||||||||||||| ||||||||    :|  |||||||||
Db     61  NEFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSTLSHY----YAMDYWGQGTS  115
           |||||| ||||:|||||||||:|||||:||||||| :|         |||||||||||
Qy    119  VTVSS  123
           |||||
Db    116  VTVSS  120
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Search completed: January 6, 2003, 13:17:29
Job time : 24.1091 secs

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              GenCore version 5.1.3
         Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:   January  6, 2003, 12:46:55 ; Search time 29.2727 Seconds
                                        (without alignments)
                                        573.557 Million cell updates/sec

Title:           US-09-155-739-2
Perfect score:   680
Sequence:        1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:          908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_101002:*
         1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
         2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	100.0	126	16	AAR81326	Mouse VLA-4 antibo
2	680	100.0	126	16	AAR81332	Human VLA-4 reshap
3	680	100.0	126	18	AAW22409	Alpha-4 integrin m
4	634	93.2	128	15	AAR60627	MEl-14 light chain
5	619	91.0	126	18	AAW22419	Humanised alpha-4
6	618.5	91.0	128	11	AAR06252	Variable region of
7	569	83.7	106	16	AAR81328	Mouse anti-VLA-4 a
8	539	79.3	359	20	AAY29913	Human MCP-3 and mu
9	539	79.3	361	20	AAY29911	Human IP-10 and mu
10	535	78.7	374	20	AAY29916	Artificial synthet
11	510.5	75.1	107	16	AAR78970	Light chain variab
12	508	74.7	106	16	AAR81321	Humanized anti-VLA
13	508	74.7	106	18	AAW22412	Humanised alpha-4
14	508	74.7	108	17	AAR93159	Murine monoclonal
15	508	74.7	637	13	AAR26983	(FRP51)-ETA fusion
16	507	74.6	245	19	AAW26800	Anti-gp54 MAb T16
17	503	74.0	109	19	AAW26797	Anti-gp54 MAb T16
18	503	74.0	240	16	AAR85495	ScFv(FWP51). Synt
19	501	73.7	355	18	AAW35113	R. piplens recombi
20	500	73.5	109	12	AAR13658	Murine OKT4A light
21	500	73.5	241	13	AAR26981	FWP51 fusion prote
22	479.5	70.5	234	12	AAR13050	CD4-specific CDR-g
23	464.5	68.3	128	22	AABB1995	Ganglioside GD3 sp
24	462.5	68.0	234	18	AAW10233	TF8-5G9 CDR-grafte
25	458.5	67.4	260	23	ABP41164	Human ovarian anti
26	457.5	67.3	128	22	AABB1996	Ganglioside GD3 sp
27	456.5	67.1	129	15	AAR57482	Humanised 1308F VL
28	456.5	67.1	129	17	AAR92085	Humanised antibody
29	455.5	67.0	129	15	AAR47207	Human/murine IL-1
30	452.5	66.5	128	22	AABB1997	Ganglioside GD3 sp
31	451.5	66.4	127	12	AAR12359	Light (kappa) chai
32	451.5	66.4	129	21	AAY56724	Amino acid sequenc
33	448.5	66.0	128	22	AABB1993	Ganglioside GD3 sp
34	447.5	65.8	129	19	AAW70379	Anti-human CD23 5E
35	446.5	65.7	126	12	AAR12237	Mouse MAb 1C11 L c
36	446.5	65.7	129	14	AAR30880	pXOM2. Mus muscul
37	445.5	65.5	132	18	AAW22842	Human anti-tumour
38	443.5	65.2	130	21	AAY56737	Amino acid sequenc
39	442.5	65.1	236	23	AAU74297	Anti-human AILIM m
40	442	65.0	124	21	AAY56719	Amino acid sequenc
41	441	64.9	237	21	AAY96301	Human IGFAM-13 imm
42	441	64.9	241	22	AAB82912	Human immune respo
43	440.5	64.8	129	23	ABG35326	Thrombopoletin ago
44	440.5	64.8	134	23	AAM47645	Human protein sequ
45	438.5	64.5	128	17	AAW01527	Monoclonal antibod

ALIGNMENTS

```
RESULT 1
AAR81326
ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
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PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;

Query Match        100.0%;   Score 680;  DB 16;   Length 126;
Best Local Similarity   100.0%;   Pred. No. 2.1e-47;
Matches  126;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP  60
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Db     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP  60

Qy    61  GKPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GKPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG  120

Qy   121  TKLEIK  126
          ||||||
Db   121  TKLEIK  126

RESULT 2
AAR81332
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using mammalian cell PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions.  In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis.  They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis.  The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;

Query Match        100.0%;   Score 680;  DB 16;   Length 126;
Best Local Similarity   100.0%;   Pred. No. 2.1e-47;
Matches  126;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP  60

Qy    61  GKPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GKPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG  120
```

```
Qy    121 TKLEIK 126
          ||||||
Db    121 TKLEIK 126

RESULT 3
AAW22409
ID    AAW22409 standard; Protein; 126 AA.
XX
AC    AAW22409;
XX
DT    08-DEC-1997  (first entry)
XX
DE    Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW    asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW    metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW    transplant rejection; graft versus host disease; nephritis;
KW    atopic dermatitis; psoriasis; myocardial ischaemia;
KW    acute leukocyte mediated lung injury; therapy.
XX
OS    Mus musculus.
XX
FH    Key             Location/Qualifiers
FT    Peptide         1..20
FT                    /label= Leader
FT    Region          21..43
FT                    /label= FR1
FT                    /note= "framework region 1"
FT    Region          44..54
FT                    /label= CDR1
FT                    /note= "complementarity determining region 1"
FT    Region          55..69
FT                    /label= FR2
FT                    /note= "framework region 2"
FT    Region          70..76
FT                    /label= CDR2
FT                    /note= "complementarity determining region 2"
FT    Region          77..108
FT                    /label= FR3
FT                    /note= "framework region 3"
FT    Region          109..116
FT                    /label= CDR3
FT                    /note= "complementarity determining region 3"
FT    Region          117..126
FT                    /label= FR4
FT                    /note= "framework region 4"
XX
PN    WO9718838-A1.
XX
PD    29-MAY-1997.
XX
PF    21-NOV-1996;  96WO-US18807.
XX
PR    21-NOV-1995;  95US-0561521.
XX
PA    (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI    Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR    WPI; 1997-297879/27.
DR    N-PSDB; AAT74759.
XX
PT    Uses of humanised alpha-4 integrin antibody - for treatment of
PT    asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS    Claim 18; Page 68; 107pp; English.
XX
CC    This polypeptide comprises the light chain variable region (VL) of
CC    mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC    complementarity determining regions (CDRs) of the 21.6 VL can be
CC    incorporated into a human REI framework to produce a claimed
CC    humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC    antibody that is used in the manufacture of a medicament for
CC    treating a disease selected from asthma, atherosclerosis, AIDS,
CC    dementia, diabetes, inflammatory bowel disease, rheumatoid
CC    arthritis, transplant rejection, graft versus host disease, tumour
CC    metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC    ischaemia, and acute leukocyte mediated lung injury. The antibody
CC    may also be used in the affinity purification of alpha-4 integrin
CC    for use as a vaccine or an immunogen. It is also useful for
CC    generating idiotypic antibodies. The humanised antibodies of the
CC    invention have a half-life in the human circulation essentially
CC    equivalent to that of naturally occurring human antibodies.
XX
SQ    Sequence  126 AA;

Query Match             100.0%;  Score 680;  DB 18;  Length 126;
Best Local Similarity   100.0%;  Pred. No. 2.1e-47;
Matches 126;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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Db    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGG 120

Qy  121 TKLEIK 126
          ||||||
Db  121 TKLEIK 126

RESULT 4
AAR60627
ID    AAR60627 standard; Protein; 128 AA.
XX
AC    AAR60627;
XX
DT    04-JUN-1995  (first entry)
XX
DE    MEl-14 light chain variable region.
XX
KW    Monoclonal antibody; tumour.
XX
OS    Homo sapiens.
XX
PN    WO9421294-A.
XX
PD    29-SEP-1994.
XX
PF    14-MAR-1994;  94WO-US02724.
XX
PR    19-MAR-1993;  93US-0033864.
XX
PA    (BIGN/) BIGNER D D.
PA    (CARR/) CARREL S.
PA    (ZALU/) ZALUTSKY M R.
XX
PI    Bigner DD, Carrel S, Zalutsky MR;
XX
DR    WPI; 1994-316669/39.
DR    N-PSDB; AAQ73537.
XX
PT    Method of treating solid or cystic tumours with antibodies - by
PT    administering monoclonal antibody Mel-14, having Fc deleted,
PT    using injection or deposition in the cyst cavity
XX
PS    Disclosure; Fig 2; 31pp; English.
XX
CC    The sequence is that of the MEl-14 light chain. The protein is a
CC    monoclonal antibody which can be administered to treat solid or
CC    cystic tumours.
CC    See also AAR60626.
```

XX
SQ   Sequence   128 AA;

Query Match   93.2%;   Score 634; DB 15;   Length 128;
Best Local Similarity   93.7%;   Pred. No. 1e-43;
Matches 118; Conservative   3; Mismatches   5; Indels   0; Gaps   0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   1 MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
        ||||||||||||||||||||||||||||||||:|||||||||||||||||||||| ||||
Db   61 GKGPRLLMHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGG 120

Qy 121 TKLEIK 126
        ||||||
Db 121 TKLEIK 126

RESULT 5
AAW22419
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..20
FT   /label= Leader
FT   Protein   21..126
FT   /label= Mat_protein
FT   /note= "VL version La (Claim 25)"
FT   Region   21..43
FT   /label= FR1
FT   /note= "REI framework region 1"
FT   Region   44..54
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   55..69
FT   /label= FR2
FT   /note= "REI framework region 2"
FT   Region   70..76
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   77..108
FT   /label= FR3
FT   /note= "REI framework region 3"
FT   Region   109..116
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
FT   Region   117..126
FT   /label= FR4
FT   /note= "REI framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX

XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412). It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;

Query Match   91.0%;   Score 619; DB 18;   Length 126;
Best Local Similarity   90.5%;   Pred. No. 1.6e-42;
Matches 114; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
        | ||||||||||||||||||||||||||||||||||||||||| :||||||||||||||
Db   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASVGDRVTITCKASQDINKYMAWYQQTP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   61 GKAPRLLIHYTSALQPGIPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLLTFGGG 120

Qy 121 TKLEIK 126
        ||:|||
Db 121 TKVEIK 126

RESULT 6
AAR06252
ID   AAR06252 standard; protein; 128 AA.
XX
AC   AAR06252;
XX
DT   10-DEC-1990 (first entry)
XX
DE   Variable region of murine AHT 107 light chain.
XX
KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
XX
PF   24-JAN-1990;   90EP-0101351.
XX
PR   04-DEC-1989;   89US-0441702.

```
PR   24-JAN-1989;  89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zerler B;
XX
DR   WPI; 1990-232892/31.
DR   N-PSDB; AAQ05556.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
PS   Disclosure; ; p; English.
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence  128 AA;

     Query Match             91.0%;  Score 618.5;  DB 11;  Length 128;
     Best Local Similarity   88.2%;  Pred. NO. 1.8e-42;
     Matches  112;  Conservative  12;  Mismatches  2;  Indels  1;  Gaps  1;

Qy     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP  60
          |||||||||||||||||||||||||||||||||||||||||||||::|||||||||||||
Db     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKFIAWYQHKP  60

Qy    61  GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG  119
          :.|||||||||||||||||||||||||||||::|||||||||||||||:|:| |||||
Db    61  GEGPRLIIHYTSTLQPGIPSRFSGSGSGKDYSFSINNLEPEDIATYYCLRYDDLPWTFGG  120

Qy   120  GTKLEIK  126
          |||||::
Db   121  GTKLEVR  127

RESULT 7
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Region         1..23
FT                  /label= FR1
FT                  /note= "mouse light chain variable framework
FT                  region 1"
FT   Region         24..34
FT                  /label= CDR1
FT                  /note= "mouse light chain variable complementarity
FT                  determining region 1"
FT   Region         35..49
FT                  /label= FR2
FT                  /note= "mouse light chain variable framework
FT                  region 2"
FT   Region         50..56
FT                  /label= CDR2
FT                  /note= "mouse light chain variable complementarity
FT                  determining region 2"
FT   Region         57..88
FT                  /label= FR3
FT                  /note= "mouse light chain variable framework
FT   Region         89..96           region 3"
FT                  /label= CDR3
FT                  /note= "mouse light chain variable complementarity
FT                  determining region 3"
FT   Region         97..106
FT                  /label= FR4
FT                  /note= "mouse light chain variable framework
FT                  region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain, in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  106 AA;

     Query Match             83.7%;  Score 569;  DB 16;  Length 106;
     Best Local Similarity  100.0%;  Pred. No. 1.4e-38;
     Matches  106;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  60

Qy    81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK  126
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    61  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK  106

RESULT 8
AAY29913
ID   AAY29913 standard; Protein; 359 AA.
XX
AC   AAY29913;
XX
DT   17-NOV-1999  (first entry)
XX
DE   Human MCP-3 and murine scFv38 fusion protein.
```

```
XX
KW  Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW  immune response; HIV; infection.
XX
OS  Homo sapiens.
OS  Mus sp.
OS  Synthetic.
XX
PN  WO9946392-A1.
XX
PD  16-SEP-1999.
XX
PF  12-MAR-1999;    99WO-US05345.
XX
PR  12-MAR-1998;    98US-0077745.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Kwak LW, Biragyn A;
XX
DR  WPI; 1999-551418/46.
XX
PT  New fusion polypeptides comprising a chemokine and a tumour antigen or
PT  HIV antigen, used for treating cancers or treating or preventing HIV
PT  infection -
XX
PS  Disclosure; Page 118-119; 142pp; English.
XX
CC  The present invention describes fusion proteins comprising a chemokine
CC  and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC  comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC  Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC  (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC  SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC  HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC  gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC  be used for producing an immune response, e.g. an effector T cell immune
CC  response. They can also be used for treating cancer or treating or
CC  preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC  can be used in in vitro diagnostic assays, as well as in screening assays
CC  for identifying unknown tumour antigen epitopes and fine mapping of
CC  tumour antigen epitopes. The present sequence represents a fusion protein
CC  from the present invention.
XX
SQ  Sequence   359 AA;

Query Match             79.3%;   Score 539;  DB 20;  Length 359;
Best Local Similarity   91.8%;   Pred. No. 1.2e-35;
Matches  101;  Conservative    4;  Mismatches    5;   Indels    0;  Gaps    0;

Qy     17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |:||||||||||||||||||||||||||:||||||||||  |||||||||||||||||
Db    229 GSGSDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQP 288

Qy     77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||:||||||||||||||||||:||||||||||
Db    289 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 338

RESULT 9
AAY29911
ID  AAY29911 standard; Protein; 361 AA.
XX
AC  AAY29911;
XX
DT  17-NOV-1999  (first entry)
XX
DE  Human IP-10 and murine scFv38 fusion protein.
XX
KW  Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW  immune response; HIV; infection.
XX
OS  Homo sapiens.
```

```
OS  Mus sp.
OS  Synthetic.
XX
PN  WO9946392-A1.
XX
PD  16-SEP-1999.
XX
PF  12-MAR-1999;    99WO-US05345.
XX
PR  12-MAR-1998;    98US-0077745.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Kwak LW, Biragyn A;
XX
DR  WPI; 1999-551418/46.
XX
PT  New fusion polypeptides comprising a chemokine and a tumour antigen or
PT  HIV antigen, used for treating cancers or treating or preventing HIV
PT  infection -
XX
PS  Disclosure; Page 115-116; 142pp; English.
XX
CC  The present invention describes fusion proteins comprising a chemokine
CC  and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC  comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC  Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC  (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC  SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC  HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC  gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC  be used for producing an immune response, e.g. an effector T cell immune
CC  response. They can also be used for treating cancer or treating or
CC  preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC  can be used in in vitro diagnostic assays, as well as in screening assays
CC  for identifying unknown tumour antigen epitopes and fine mapping of
CC  tumour antigen epitopes. The present sequence represents a fusion protein
CC  from the present invention.
XX
SQ  Sequence   361 AA;

Query Match             79.3%;   Score 539;  DB 20;  Length 361;
Best Local Similarity   91.8%;   Pred. No. 1.2e-35;
Matches  101;  Conservative    4;  Mismatches    5;   Indels    0;  Gaps    0;

Qy     17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |:||||||||||||||||||||||||||:||||||||||  |||||||||||||||||
Db    231 GSGSDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQP 290

Qy     77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||:||||||||||||||||||:||||||||||
Db    291 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 340

RESULT 10
AAY29916
ID  AAY29916 standard; Protein; 374 AA.
XX
AC  AAY29916;
XX
DT  17-NOV-1999  (first entry)
XX
DE  Artificial synthetic construct protein SEQ ID NO:15.
XX
KW  Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW  immune response; HIV; infection.
XX
OS  Synthetic.
XX
PN  WO9946392-A1.
XX
PD  16-SEP-1999.
XX
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PF　12-MAR-1999;　99WO-US05345.
XX
PR　12-MAR-1998;　98US-0077745.
XX
PA　(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI　Kwak LW, Biragyn A;
XX
DR　WPI; 1999-551418/46.
XX
PT　New fusion polypeptides comprising a chemokine and a tumour antigen or
PT　HIV antigen, used for treating cancers or treating or preventing HIV
PT　infection -
XX
PS　Disclosure; Page 117-118; 142pp; English.
XX
CC　The present invention describes fusion proteins comprising a chemokine
CC　and a tumour antigen or HIV antigen. Specifically claimed fusion
CC　proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC　human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC　Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC　human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC　MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC　HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC　can be used for producing an immune response, e.g. an effector T cell
CC　immune response. They can also be used for treating cancer or treating
CC　or preventing HIV infection. The fusion proteins and/or nucleotide
CC　sequences can be used in in vitro diagnostic assays, as well as in
CC　screening assays for identifying unknown tumour antigen epitopes and fine
CC　mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC　sequences given in the SEQ ID LISTING in the present invention but which
CC　are not mentioned further within the specification.
XX
SQ　Sequence　374 AA;

Query Match　78.7%;　Score 535;　DB 20;　Length 374;
Best Local Similarity　94.3%;　Pred. No. 2.6e-35;
Matches　100;　Conservative　3;　Mismatches　3;　Indels　0;　Gaps　0;

Qy　21　DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
　　　　　|||||||||||||||||||||||| |||||| |||||||| ||||||||| ||||||||
Db　95　DIQMTQSPSSLSASLGGKVTITCKASODINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 154

Qy　81　RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
　　　　　||||||||||||||| |||||||||||||||||||| ||||||||||
Db　155　RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200

RESULT 11
AAR78970
ID　AAR78970 standard; Protein; 107 AA.
XX
AC　AAR78970;
XX
DT　21-DEC-1995 (first entry)
XX
DE　Light chain variable region for monoclonal antibody 23F8.
XX
KW　Monoclonal antibody; heavy metal; mercury; variable region;
KW　light chain.
XX
OS　Synthetic.
XX
PN　WO9520607-A.
XX
PD　03-AUG-1995.
XX
PF　27-JAN-1995;　95WO-US01199.
XX
PR　27-JAN-1994;　94US-0187407.
XX
PA　(BION-) BIONEBRASKA INC.
XX

PI　Lopez O, Wagner FW, Wylie DE;
XX
DR　WPI; 1995-275415/36.
DR　N-PSDB; AAQ97508.
XX
PT　New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT　monoclonal antibodies, used for detecting, removing, adding or
PT　neutralising heavy metals
XX
PS　Claim 23; Page 67-68; 106pp; English.
XX
CC　Hybridoma antibodies have been produced with the spleen cells of
CC　BALB/c mouse that had received multiple injections of mercuric ions
CC　reacted with glutathione to produce a mercuric ion coordinate
CC　covalent compound which was covalently bound to keyhole limpet
CC　hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC　5B6 and 3E8) were producing MAbs that were strongly positive
CC　against glutathione-mercuric ions but negative against glutathione
CC　without mercuric ions. RNA was isolated from hybridoma cells with
CC　guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC　by MuIv reverse transcriptase. The primers used for cDNA synthesis
CC　were complementary to the 5' end of the CH1 domain of the heavy
CC　chain expressed by the hybridoma of interest, or to the 5' and of
CC　the C kappa domain. Some of the primers used for cDNA synthesis are
CC　shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC　variable region of a particular antibody polypeptide was also used
CC　for PCR amplification of that variable region, in conjunction with
CC　an appropriate V-region primer. In addition, the VH primer AAQ97518
CC　was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC　of the PCR amplified nucleotides were determined. These are given
CC　in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC　AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC　and in the claims are different from the descriptions in the
CC　sequence listings. The descriptions in the sequence listings are
CC　used here.
XX
SQ　Sequence　107 AA;

Query Match　75.1%;　Score 510.5;　DB 16;　Length 107;
Best Local Similarity　91.6%;　Pred. No. 7e-34;
Matches　98;　Conservative　3;　Mismatches　5;　Indels　1;　Gaps　1;

Qy　21　DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
　　　　　|||||||||||||||||||||||| |||||| |||||| ||||||||| ||||||||
Db　1　DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy　81　RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
　　　　　|||||||||||||| :||| ||||||||||||| :-||:|||||||||
Db　61　RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGGSGTKLEIK 107

RESULT 12
AAR81321
ID　AAR81321 standard; Protein; 106 AA.
XX
AC　AAR81321;
XX
DT　02-APR-1996 (first entry)
XX
DE　Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW　Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW　antibody engineering.
XX
OS　Chimeric Mus musculus.
OS　Chimeric Homo sapiens.
XX
PN　WO9519790-A1.
XX
PD　27-JUL-1995.
XX
PF　25-JAN-1995;　95WO-US01219.
XX

```
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanised antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (See
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence 106 AA;

Query Match      74.7%;    Score 508;   DB 16;   Length 106;
Best Local Similarity   88.7%;
Matches  94;   Conservative   6;   Mismatches   6;   Indels   0;   Gaps   0;

Qy     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          |||||||||||||| :||||||||||||||||| :||||||||||||||||||||||||||
Db      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||| ||:|:|||||||||||||||||||||| ||||:|||
Db     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT 13
AAW22412
ID   AAW22412 standard; Protein; 106 AA.
XX
AC   AAW22412;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key            Location/Qualifiers
FT   Region         1..23
FT                  /label= FR1
FT                  /note= "REI framework region 1"
FT   Region         24..34
FT                  /label= CDR1
FT                  /note= "21.6 complementarity determining region 1"
FT   Region         35..49
FT                  /label= FR2
FT                  /note= "REI framework region 2"
FT   Misc-difference 45
FT                  /note= "REI Lys-45 is substd. by Lys of mouse
FT                  21.6 VL, important in supporting the
FT                  CDR2 loop"
FT   Misc-difference 49
FT                  /note= "REI Tyr-49 is substd. by His of mouse
FT                  21.6 VL, located at the binding site"
FT   Region         50..56
FT                  /label= CDR2
FT                  /note= "21.6 complementarity determining region 2"
FT   Region         57..88
FT                  /label= FR3
FT                  /note= "REI framework region 3"
FT   Misc-difference 58
FT                  /note= "REI Val-58 is substd. by Ile of mouse
FT                  21.6 VL, important in supporting the CDR2
FT                  loop"
FT   Misc-difference 69
FT                  /note= "REI Thr-69 is substd. by Arg of mouse
FT                  21.6 VL, involved in antibody-antigen
FT                  binding"
FT   Region         89..96
FT                  /label= CDR3
FT                  /note= "21.6 complementarity determining region 3"
FT   Region         97..106
FT                  /label= FR4
FT                  /note= "REI framework region 4"
FT   Misc-difference 103
FT                  /note= "REI Leu-103 substd. by Val, more typical
FT                  of human kappa light chain J region"
FT   Misc-difference 104
FT                  /note= "REI Gln-104 substd. by Glu, more typical
FT                  of human kappa light chain J region"
FT   Misc-difference 106
FT                  /note= "REI Thr-106 substd. by Lys, more typical
FT                  of human kappa light chain J region"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 6; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
```

```
CC  arthritis, transplant rejection, graft versus host disease, tumour
CC  metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC  ischaemia, and acute leukocyte mediated lung injury. The antibody
CC  may also be used in the affinity purification of alpha-4 integrin
CC  for use as a vaccine or an immunogen. It is also useful for
CC  generating idiotypic antibodies. The humanised antibody has a
CC  half-life in the human circulation essentially equivalent to that
CC  of naturally occurring human antibodies.
XX
SQ  Sequence  106 AA;

Query Match             74.7%;  Score 508; DB 18; Length 106;
Best Local Similarity   88.7%;  Pred. No. 1.1e-33;
Matches     94; Conservative    6; Mismatches    6; Indels    0; Gaps    0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        ||||||||||||:| :|||||||||||||||||||||| ||:||||||||||||||||||||
Db    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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Db   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKVEIK 106

RESULT 14
AAR93159
ID  AAR93159 standard; Protein; 108 AA.
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AC  AAR93159;
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DT  24-OCT-1996  (first entry)
XX
DE  Murine monoclonal antibody K20 kappa chain variable region.
XX
KW  Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW  beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW  T cell activation; complementary determining region; CDR.
XX
OS  Mus musculus.
XX
FH  Key             Location/Qualifiers
FT  Region          1..23
FT                  /label= FR1
FT                  /note= "framework region"
FT  Region          24..34
FT                  /label= CDR1
FT                  /note= "complementarity determining region"
FT  Region          35..49
FT                  /label= FR2
FT                  /note= "framework region"
FT  Region          50..56
FT                  /label= CDR2
FT                  /note= "complementarity determining region"
FT  Region          57..88
FT                  /label= FR3
FT                  /note= "framework region"
FT  Region          89..94
FT                  /label= CDR3
FT                  /note= "complementarity determining region"
FT  Region          95..108
FT                  /label= J_kappa1
XX
PN  FR2724393-A1.
XX
PD  15-MAR-1996.
XX
PF  12-SEP-1994;  94FR-0010858.
XX
PR  12-SEP-1994;  94FR-0010858.
XX
PA  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA  (PROT-) PROTEINE PERFORMANCE SA.
XX

PI  Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI  Poul MA;
XX
DR  WPI; 1996-162083/17.
DR  N-PSDB; AAT26849.
XX
PT  Humanisation of non-human immunoglobulin variable regions - for
PT  prodn. of humanised antibodies, esp. K20, e.g. as an
PT  immunosuppressant
XX
PS  Example 1; Fig 2A; 39pp; French.
XX
CC  The present sequence is that of the variable region of the kappa
CC  light chain from murine monoclonal antibody K20. The antibody
CC  recognises the beta 1 subunit (CD29) of integrins and inhibits
CC  activation and proliferation of peripheral T cells induced by
CC  anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC  for humanisation; the humanised version may be useful as an
CC  immunosuppressant. In the humanisation process, the complementarity
CC  determining regions (CDRs) of a human antibody with framework
CC  regions 70-95% homologous to those of K20 were replaced by the K20
CC  CDRs.
XX
SQ  Sequence  108 AA;

Query Match             74.7%;  Score 508; DB 17; Length 108;
Best Local Similarity   89.6%;  Pred. No. 1.1e-33;
Matches     95; Conservative    5; Mismatches    6; Indels    0; Gaps    0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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Db    1 DIQLTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHEPGKGPRLLIRYTSKLESGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYNLWTFGGGTKLEIK 106

RESULT 15
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ID  AAR26983 standard; Protein; 637 AA.
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AC  AAR26983;
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DT  11-FEB-1993  (first entry)
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DE  (FRP51)-ETA fusion protein.
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KW  Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
KW  variable region; ETA.
XX
OS  Pseudomonas aeruginosa.
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FH  Key             Location/Qualifiers
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FT                  /label= ompA_signal_peptide
FT  Peptide         22..29
FT                  /label= FLAG_peptide_and_enterokinase_cleavage_site
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FT                  /label= FWP51_heavy_chain_variable_domain
FT  Peptide         153..167
FT                  /label= Linker
FT  Domain          168..274
FT                  /label= FRP5_light_chain_variable_domain
FT  Protein         276..397
FT                  /label= ETA_252-613
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PN  EP502812-A.
XX
PD  09-SEP-1992.
XX
PF  27-JAN-1992;  92EP-0810056.
XX
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PR   05-FEB-1991; 91EP-0810079.
XX
PA   (CIBA) CIBA GEIGY AG.
XX
PI   Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI   Zwickl M;
XX
DR   WPI; 1992-302096/37.
DR   N-PSDB; AAQ28263.
XX
PT   Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT   for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT   or ovarian tumours
XX
PS   Disclosure; Page 53-58; 67pp; English.
XX
CC   The sequences given in AAR26982-3 contain part of the exotoxin A (ETA)
CC   sequence corresponding to positions 252-613 of the full exotoxin A
CC   sequence. These sequences are encoded by Fv(FRP5)-ETA fusion genes.
CC   The ETA sequence was used as a marker gene so that E. coli transformed
CC   with the fusion gene could be identified. The fusion genes were
CC   expressed in E. coli and the antibodies were extracted. These
CC   recombinant antibodies can be used for the qualitative and
CC   quantitative determination of c-erbB-2. This can be used for
CC   monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
XX
SQ   Sequence   637 AA;

Query Match   74.7%; Score 508; DB 13; Length 637;
Best Local Similarity   86.4%; Pred. No. 6.4e-33;
Matches   95; Conservative   5; Mismatches   10; Indels   0; Gaps   0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          | |||:|||||||||||||||| ||| |:||||||||| ||||||||| ||
Db   164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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Db   224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273

Search completed: January 6, 2003, 13:15:15
Job time : 31.2727 secs

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            GenCore version 5.1.3
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      January  6, 2003, 13:13:21 ; Search time 10.4364 Seconds
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                                          355.228 Million cell updates/sec

Title:         US-09-155-739-2
Perfect score: 680
Sequence:      1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      262574 seqs, 29422922 residues               262574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_AA:*
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           3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
           4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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           6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:**
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	680	100.0	126	2	US-08-561-521-2	Sequence 2, Appl1
2	680	100.0	126	2	US-08-561-521-15	Sequence 15, Appl1
3	680	100.0	126	5	PCT-US95-01219-2	Sequence 2, Appl1
4	680	100.0	126	5	PCT-US95-01219-15	Sequence 15, Appl1
5	634	93.2	128	1	US-08-339-582-4	Sequence 4, Appl1
6	569	83.7	106	2	US-08-561-521-5	Sequence 5, Appl1
7	569	83.7	106	5	PCT-US95-01219-5	Sequence 5, Appl1
8	510.5	75.1	107	2	US-08-888-366-22	Sequence 22, Appl1
9	508	74.7	106	2	US-08-561-521-7	Sequence 7, Appl1
10	508	74.7	106	5	PCT-US95-01219-7	Sequence 7, Appl1
11	508	74.7	637	1	US-08-235-838-16	Sequence 16, Appl1
12	508	74.7	637	2	US-08-465-473B-16	Sequence 16, Appl1
13	503	74.0	241	1	US-08-235-838-11	Sequence 11, Appl1
14	503	74.0	241	2	US-08-465-473B-11	Sequence 11, Appl1
15	501	73.7	355	3	US-08-875-811-57	Sequence 57, Appl1
16	438.5	64.5	128	1	US-08-259-372A-14	Sequence 14, Appl1
17	438.5	64.5	128	1	US-08-468-671-14	Sequence 14, Appl1
18	437.5	64.3	127	4	US-08-458-516-5	Sequence 5, Appl1
19	437.5	64.3	127	4	US-08-348-548-4	Sequence 4, Appl1
20	437.5	64.3	127	5	PCT-US95-15716-4	Sequence 4, Appl1
21	437.5	64.3	131	1	US-08-236-520-2	Sequence 2, Appl1
22	437.5	64.3	131	5	PCT-US95-05262-2	Sequence 2, Appl1
23	434.5	63.9	128	4	US-09-225-322B-10	Sequence 10, Appl1
24	434.5	63.9	128	4	US-09-225-322B-19	Sequence 19, Appl1
25	430.5	63.3	138	2	US-08-480-434-63	Sequence 63, Appl1
26	430.5	63.3	138	2	US-08-053-451B-63	Sequence 63, Appl1
27	429.5	63.2	127	3	US-08-836-561-71	Sequence 71, Appl1
28	428.5	63.0	129	1	US-08-217-918-2	Sequence 2, Appl1
29	426.5	62.7	127	2	US-08-137-117D-37	Sequence 37, Appl1
30	426.5	62.7	127	2	US-08-436-717-37	Sequence 37, Appl1
31	424.5	62.4	127	3	US-08-649-100-17	Sequence 17, Appl1
32	423.5	62.3	236	1	US-08-157-101A-5	Sequence 5, Appl1
33	418.5	61.5	142	2	US-08-579-940-2	Sequence 2, Appl1
34	418.5	61.5	142	4	US-08-838-692-4	Sequence 4, Appl1
35	417.5	61.4	127	2	US-08-137-117D-29	Sequence 29, Appl1
36	417.5	61.4	127	2	US-08-436-717-29	Sequence 29, Appl1
37	417.5	61.4	127	3	US-08-933-983-7	Sequence 7, Appl1
38	416.5	61.3	127	3	US-08-621-751A-6	Sequence 6, Appl1
39	416.5	61.3	127	3	US-08-836-561-88	Sequence 88, Appl1
40	414.5	61.0	128	2	US-08-470-139-26	Sequence 26, Appl1
41	414.5	61.0	128	4	US-09-347-061-26	Sequence 26, Appl1
42	413.5	60.8	125	1	US-08-039-198B-12	Sequence 12, Appl1
43	413.5	60.8	125	2	US-08-182-067-2	Sequence 2, Appl1
44	413.5	60.8	125	2	US-08-465-313-2	Sequence 2, Appl1
45	413.5	60.8	127	3	US-08-649-100-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-2

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  Best Local Similarity   100.0%; Pred. No. 1.7e-59;
  Matches 126; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 2
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-15

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Query Match             100.0%;  Score 680;  DB 2;  Length 126;
Best Local Similarity   100.0%;  Pred. No. 1.7e-59;
Matches  126;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

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RESULT 3
PCT-US95-01219-2
; Sequence 2, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-2

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Query Match             100.0%;  Score 680;  DB 5;  Length 126;
Best Local Similarity   100.0%;  Pred. No. 1.7e-59;
Matches  126;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy  121 TKLEIK 126
        ||||||
Db  121 TKLEIK 126
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RESULT 4
PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran

```
TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
TITLE OF INVENTION:  Adhesion Molecule VLA-4
NUMBER OF SEQUENCES:  45
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Townsend and Townsend Khourie and Crew
   STREET:  One Market Plaza, Steuart Tower, Suite 2000
   CITY:  San Francisco
   STATE:  California
   COUNTRY:  USA
   ZIP:  94105
COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  PCT/US95/01219
   FILING DATE:  25-JAN-1995
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 08/186,269
   FILING DATE:  25-JAN-1994
ATTORNEY/AGENT INFORMATION:
   NAME:  Smith, William L.
   REGISTRATION NUMBER:  30,223
   REFERENCE/DOCKET NUMBER:  15270-14
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  415-543-9600
   TELEFAX:  415-543-5043
INFORMATION FOR SEQ ID NO:  15:
SEQUENCE CHARACTERISTICS:
   LENGTH:  126 amino acids
   TYPE:  amino acid
   TOPOLOGY:  linear
   MOLECULE TYPE:  protein
PCT-US95-01219-15

Query Match         100.0%;   Score 680;   DB 5;   Length 126;
Best Local Similarity  100.0%;   Pred. No. 1.7e-59;   Indels  0;   Gaps  0;
Matches  126;   Conservative  0;   Mismatches  0;

Qy    1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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Db    1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy   61  GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy  121  TKLEIK 126
         ||||||
Db  121  TKLEIK 126

RESULT 5
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
; GENERAL INFORMATION:
;   APPLICANT:  Bigner, Darell D.
;   APPLICANT:  Zalutsky, Michael R.
;   APPLICANT:  Carrel, Stefan
;   TITLE OF INVENTION:  METHOD OF TREATMENT
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  North Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/08/339,582
   FILING DATE:
   CLASSIFICATION:  424
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 08/033,864
   FILING DATE:  19-MAR-1993
ATTORNEY/AGENT INFORMATION:
   NAME:  Sibley, Kenneth D.
   REGISTRATION NUMBER:  31,665
   REFERENCE/DOCKET NUMBER:  5405-89
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  919-420-2200
   TELEFAX:  919-881-3175
INFORMATION FOR SEQ ID NO:  4:
SEQUENCE CHARACTERISTICS:
   LENGTH:  128 amino acids
   TYPE:  amino acid
   TOPOLOGY:  linear
   MOLECULE TYPE:  protein
US-08-339-582-4

Query Match          93.2%;   Score 634;   DB 1;   Length 128;
Best Local Similarity   93.7%;   Pred. No. 5.4e-55;   Indels  0;   Gaps  0;
Matches  118;   Conservative  3;   Mismatches  5;

Qy    1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||||||||||||||||||:|||||||||||||||||||||||||:||||||:||||||||
Db    1  MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60

Qy   61  GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
         ||:||||:||:|||||||||||||||||||||:|||||||||||||||||||||:|||||
Db   61  GKGPRLLMHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGG 120

Qy  121  TKLEIK 126
         ||||||
Db  121  TKLEIK 126

RESULT 6
US-08-561-521-5
; Sequence 5, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT:  Bendig, Mary M.
;   APPLICANT:  Leger, Olivier J.
;   APPLICANT:  Saldanha, Jose
;   APPLICANT:  Jones, S. Tarran
;   TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION:  Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES:  45
;   CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
```

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;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William L.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 106 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-5

Query Match        83.7%;    Score 569;    DB 2;   Length 106;
Best Local Similarity  100.0%;   Pred. No. 9.8e-49;
Matches 106;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy  21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy  81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  61  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106

RESULT 7
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION:  Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend Khourie and Crew
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US95/01219
;     FILING DATE: 25-JAN-1995
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/186,269
;     FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William L.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 106 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
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PCT-US95-01219-5

Query Match        83.7%;    Score 569;    DB 5;   Length 106;
Best Local Similarity  100.0%;   Pred. No. 9.8e-49;
Matches 106;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy  21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy  81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  61  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106

RESULT 8
US-08-888-366-22
; Sequence 22, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
;   APPLICANT: Lopez, Osvaldo
;   APPLICANT: Wylie, Dwane E.
;   APPLICANT: Wagner, Fred W.
;   TITLE OF INVENTION:  Mercury Binding Polypeptides and Nucleotides Coding Therefo
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Merchant & Gould
;     STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/888,366
;     FILING DATE: 03-JUL-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/187,407
;     FILING DATE: 27-JAN-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/990,542
;     FILING DATE: 14-DEC-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/493,299
;     FILING DATE: 14-MAR-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/324,392
;     FILING DATE: 14-MAR-1989
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Carter, Charles G.
;     REGISTRATION NUMBER: 35,093
;     REFERENCE/DOCKET NUMBER: 8648.39USC1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 612-332-5300
;     TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 107 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-888-366-22

Query Match        75.1%;    Score 510.5;    DB 2;   Length 107;
Best Local Similarity  91.6%;   Pred. No. 5.2e-43;
Matches 98;   Conservative  3;   Mismatches  5;   Indels  1;   Gaps  1;

Qy  21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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Db           |||||||||||||||||||  |||||||||||||||| ||||||||||  ||||||||
           1 DIQMTQSPSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy        81 RFSGSGSGRDYSFNISNLEPEDIATYCLQYDN-LWTFGGGTKLEIK 126
             ||||||||||||:|| ||||||:|| ||:||| |:||| |||||||
Db        61 RFSGSGSGRDYSFSISNPEPEDIATYCLQYDNSLFTFGSGTKLEIK 107
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RESULT 9
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acid
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-7

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Query Match             74.7%;  Score 508;  DB 2;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 9e-43;
Matches   94;  Conservative   6;  Mismatches   6;  Indels   0;  Gaps   0;

Qy        21 DIQMTQSPSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
             |||||||||||:: :|||||||||||||||||| ||| |||||||||||||||||||||
Db         1 DIQMTQSPSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy        81 RFSGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGGTKLEIK 126
             ||||||||||||:| ||:|||||||||||||||||| |||:||
Db        61 RFSGSGSGRDYTFTISSLQPEDIATYCLQYDNLWTFGQGTKVEIK 106
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RESULT 10
PCT-US95-01219-7
; Sequence 7, Application PCT/US9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-7

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Query Match             74.7%;  Score 508;  DB 5;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 9e-43;
Matches   94;  Conservative   6;  Mismatches   6;  Indels   0;  Gaps   0;

Qy        21 DIQMTQSPSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
             |||||||||||:: :|||||||||||||||||| ||| |||||||||||||||||||||
Db         1 DIQMTQSPSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy        81 RFSGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGGTKLEIK 126
             ||||||||||||:| ||:|||||||||||||||||| |||:||
Db        61 RFSGSGSGRDYTFTISSLQPEDIATYCLQYDNLWTFGQGTKVEIK 106
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RESULT 11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
;   APPLICANT: Wels, Winfried S.
;   APPLICANT: Hynes, Nancy E.
;   APPLICANT: Harwerth, Ina-Maria
;   APPLICANT: Groner, Bernd
;   APPLICANT: Hardman, No. 5571894man
;   APPLICANT: Zwickl, Markus
;   TITLE OF INVENTION: Recombinant Antibodies Specific for a
;   TITLE OF INVENTION: Growth Factor Receptor
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CIBA-GEIGY Corporation
;   STREET: 7 Skyline Drive
;   CITY: Hawthorne
;   STATE: New York

```
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-838-16

Query Match       74.7%;      Score 508; DB 1; Length 637;
Best Local Similarity  86.4%;    Pred. No. 7.5e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
        |||| ||:|||||||||||||| |||:||:|||||||  :|||||||||| |||||||:||
Db  164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        |||||||||||||||||:| ||||||||||| || :|||||||||||||
Db  224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273

RESULT 12
US-08-465-473B-16
; Sequence 16, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, NO. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
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FILING DATE: 5 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-473B-16

Query Match       74.7%;      Score 508; DB 2; Length 637;
Best Local Similarity  86.4%;    Pred. No. 7.5e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
        |||| ||:|||||||||||||| |||:||:|||||||  :|||||||||| |||||||:||
Db  164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        |||||||||||||||||:| ||||||||||| || :|||||||||||||
Db  224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273

RESULT 13
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
```

```
;       NAME: Elmer, James Scott
;       REGISTRATION NUMBER: 36,129
;       REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (919)541-8614
;          TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 241 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-235-838-11

Query Match             74.0%;  Score 503;  DB 1;  Length 241;
Best Local Similarity   86.2%;  Pred. No. 7.3e-42;
Matches   94;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          | ||:|||||||||||:||||||:|||||||| |||| |||||||||  ||||||||||| |||
Db   133 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 192

Qy    77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
          ||||||||||||||||:||||||||:|||||||| |:|||||||||||
Db   193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT 14
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
;       GENERAL INFORMATION:
;          APPLICANT: Wels, Winfried S.
;          APPLICANT: Hynes, Nancy E.
;          APPLICANT: Harwerth, Ina-Maria
;          APPLICANT: Groner, Bernd
;          APPLICANT: Hardman, No. 5939531man
;          APPLICANT: Zwickl, Markus
;       TITLE OF INVENTION: Recombinant Antibodies Specific for a
;       TITLE OF INVENTION: Growth Factor Receptor
;       NUMBER OF SEQUENCES: 34
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: NOVARTIS Corporation
;          STREET: 564 Morris Avenue
;          CITY: Summit
;          STATE: New Jersey
;          COUNTRY: USA
;          ZIP: 07901-6940
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/465,473B
;          FILING DATE: 5 June 1995
;          CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 07/828,832
;          FILING DATE: 31-JAN-1992
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: GB 91-810079.3
;          FILING DATE: 05-FEB-1991
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Pfeiffer, Hesna J.
;          REGISTRATION NUMBER: 22,640
;          REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (908)522 6940
;          TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 241 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-465-473B-11

Query Match             74.0%;  Score 503;  DB 2;  Length 241;
Best Local Similarity   86.2%;  Pred. No. 7.3e-42;
Matches   94;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Qy    77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
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Db   193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT 15
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
;       GENERAL INFORMATION:
;          APPLICANT: Rybak, Susanna M.
;          APPLICANT: Newton, Dianne L.
;          APPLICANT: Boque, Lluis
;          APPLICANT: Wlodawer, Alexander
;       TITLE OF INVENTION: Recombinant Ribonuclease Proteins
;       NUMBER OF SEQUENCES: 64
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Townsend and Townsend and Crew LLP
;          STREET: Two Embarcadero Center, Eighth Floor
;          CITY: San Francisco
;          STATE: California
;          COUNTRY: USA
;          ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/875,811
;          FILING DATE: 19-FEB-1998
;          CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: WO PCT/US97/02588
;          FILING DATE: 19-FEB-1997
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 60/011,800
;          FILING DATE: 21-FEB-1996
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Faris, Susan K.
;          REGISTRATION NUMBER: 41,739
;          REFERENCE/DOCKET NUMBER: 015280-244100US
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 576-0200
;          TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 355 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-875-811-57

Query Match             73.7%;  Score 501;  DB 3;  Length 355;
Best Local Similarity   86.4%;  Pred. No. 1.8e-41;
Matches   95;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

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Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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Db   305 GIPSRFSGSGSGEEYSFSISNLEPEDIATYYCQQYDNLRTFGGGTKLELK 354

Search completed: January 6, 2003, 13:19:07
Job time : 11.4364 secs

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.
Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may requests that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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                GenCore version 5.1.3
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     January  6, 2003, 13:17:36 ; Search time 6.10909 Seconds
                                          (without alignments)
                                390.875 Million cell updates/sec

Title:      US-09-155-739-2
Perfect score: 680
Sequence:   1 MRPSIQFGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched:   117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters:    117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
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    2:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
    3:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
    4:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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    6:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
    7:  /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
    8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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   10:  /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	490	72.1	109	10	US-09-229-200A-7	Sequence 7, Appl
2	482.5	71.0	108	10	US-09-229-200A-17	Sequence 17, Appl
3	442.5	65.1	236	10	US-09-859-053-30	Sequence 30, App
4	437.5	64.3	131	1	US-08-779-784-21	Sequence 21, Appl
5	435.5	64.0	234	10	US-09-740-002-24	Sequence 24, Appl
6	434.5	63.9	128	10	US-09-764-304-10	Sequence 10, Appl
7	434.5	63.9	128	10	US-09-764-304-19	Sequence 19, Appl
8	431.5	63.5	108	10	US-09-229-200A-11	Sequence 11, Appl
9	431.5	63.5	108	10	US-09-229-200A-15	Sequence 15, Appl
10	431.5	63.5	108	10	US-09-229-200A-16	Sequence 16, Appl
11	420.5	61.8	234	10	US-09-800-729-150	Sequence 150, App
12	418.5	61.5	142	10	US-09-797-481-2	Sequence 2, Appli
13	418.5	61.5	142	10	US-09-844-736-4	Sequence 4, Appli
14	416	61.2	234	10	US-09-740-002-26	Sequence 26, Appl
15	414.5	61.0	128	10	US-09-855-271-26	Sequence 26, Appl
16	413.5	60.8	125	10	US-09-809-739-1	Sequence 1, Appli
17	413	60.7	237	10	US-09-056-160B-100	Sequence 100, App
18	413	60.7	491	12	US-10-011-125-2	Sequence 2, Appli
19	411.5	60.5	108	10	US-09-905-243-73	Sequence 73, Appl
20	407.5	59.9	107	10	US-09-056-160B-15	Sequence 15, Appl
21	407	59.9	235	10	US-09-800-729-152	Sequence 152, App
22	405	59.6	237	10	US-09-940-166A-6	Sequence 6, Appli
23	404.5	59.5	110	10	US-09-056-160B-103	Sequence 103, App
24	403.5	59.3	107	10	US-09-056-160B-13	Sequence 13, Appl
25	402.5	59.2	108	10	US-09-056-160B-12	Sequence 12, Appl
26	402.5	59.0	109	10	US-09-811-123-6	Sequence 6, Appli
27	401.5	59.0	110	10	US-09-056-160B-105	Sequence 105, App
28	401.5	59.0	127	10	US-09-809-739-10	Sequence 10, Appl
29	400.5	58.9	108	9	US-10-153-159-2	Sequence 2, Appli
30	400.5	58.9	108	9	US-10-153-159-16	Sequence 16, Appl
31	400.5	58.9	108	10	US-09-056-160B-8	Sequence 8, Appli
32	399.5	58.8	107	9	US-09-253-794-6	Sequence 6, Appli
33	397.5	58.5	108	9	US-10-153-159-4	Sequence 4, Appli
34	397.5	58.5	110	10	US-09-056-160B-107	Sequence 107, App
35	397.5	58.5	110	10	US-09-056-160B-117	Sequence 117, App
36	396.5	58.3	214	10	US-09-940-166A-2	Sequence 2, Appli
37	396.5	58.3	214	10	US-09-811-384-11	Sequence 11, Appl
38	396.5	58.3	267	10	US-09-766-543-10	Sequence 10, Appl
39	395.5	58.2	107	9	US-09-999-025-15	Sequence 15, Appl
40	395.5	58.2	107	9	US-09-999-040-15	Sequence 15, Appl
41	395.5	58.2	108	10	US-09-229-200A-14	Sequence 14, Appl
42	394.5	58.0	108	10	US-09-056-160B-126	Sequence 126, App
43	393	57.8	232	9	US-10-006-771A-6	Sequence 6, Appli
44	393	57.8	443	9	US-10-006-771A-2	Sequence 2, Appli
45	393	57.8	443	12	US-10-006-773-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-09-229-200A-7
; Sequence 7, Application US/09229200A
; Patent No. US20020099179A1
GENERAL INFORMATION:
   APPLICANT: Jolliffe et al.
   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
   NUMBER OF SEQUENCES: 28
   CORRESPONDENCE ADDRESS:
       ADDRESSEE: Johnson & Johnson
       STREET: One Johnson & Johnson Plaza
       CITY: New Brunswick
       STATE: NJ
       COUNTRY: USA
       ZIP: 08933-7003
   COMPUTER READABLE FORM:
       MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
       COMPUTER: IBM
       OPERATING SYSTEM: PC-DOS
       SOFTWARE: <Unknown>
   CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/09/229,200A
       FILING DATE: 13-Jan-1999
       CLASSIFICATION: <Unknown>
   ATTORNEY/AGENT INFORMATION:
       NAME: John W. Wallen, III
       REGISTRATION NUMBER: 35,403
       REFERENCE/DOCKET NUMBER: ORT-948
   TELECOMMUNICATION INFORMATION:
       TELEPHONE: (858) 784-3239
       TELEFAX: (908) 524-2808
   INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 109
           TYPE: amino acid
           TOPOLOGY: linear
       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-200A-7

   Query Match        72.1%;  Score 490;  DB 10;  Length 109;
   Best Local Similarity  86.1%;  Pred. No. 8.8e-34;
   Matches 93;  Conservative 8;  Mismatches 5;  Indels 2;  Gaps 1;
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Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
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Db    1 DIQMTQSPSSLSASLGGKVTIACKASQDINNYIAWYQHKPGKGPRLLIHYTSTLQPGIPS  60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
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Db   61 RFSGSGSGRDYSFSISNLEPEDIATYCIQYNDLFLTTFGGGTKLEIK 108
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RESULT 2
US-09-229-200A-17
; Sequence 17, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 17
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 17
US-09-229-200A-17

Query Match   71.0%;   Score 482.5;   DB 10;   Length 108;
Best Local Similarity   87.9%;   Pred. No. 3.6e-33;
Matches 94; Conservative   3; Mismatches   9; Indels   1; Gaps   1;

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Db    1 DIQMTQSPSSLSASLGGKVTIACKASQDINNYIAWYQHKPGKGPRLLIHYTSTLQPGIPS  60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
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Db   61 RFSGSGSGRDYSFSISNLEPEDIATYCLQQYDNLLFTFGGGTKLEIK 107
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RESULT 3
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. US2002010265A1
; GENERAL INFORMATION:
;   APPLICANT: Tsuji, Takashi
;   APPLICANT: Tezuka, Katsunari
;   APPLICANT: Hori, No. US2002010265A1uaki
;   TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;   TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;   TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match   65.1%;   Score 442.5;   DB 10;   Length 236;
Best Local Similarity   64.6%;   Pred. No. 1.4e-29;
Matches 82; Conservative 20; Mismatches 24; Indels   1; Gaps   1;

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Db    3 MRVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKP  62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         ||:|:|||  :||:|| |||| :|:||||||||||: ::||:||||||| |:  :||  :||||
Db   63 GKAPKLLIYASSLQSCVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQ 122

Qy  120 GTKLEIK 126
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Db  123 GTKVEIK 129
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RESULT 4
US-08-779-784-21
; Sequence 21, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
;   APPLICANT: Rodriguez, Moses
;   APPLICANT: Miller, David J.
;   APPLICANT: Asakura, Kunihiko
;   TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
;   TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: David A. Jackson, Esq.
;   STREET: 411 Hackensack Ave, Continental Plaza, 4th
;   STREET: Floor
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/779,784
;   FILING DATE: 07-JAN-1997
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/692,084
;   FILING DATE: 08-AUG-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/236,520
;   FILING DATE: 29-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684

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;   INFORMATION FOR SEQ ID NO:   21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  131 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-779-784-21

Query Match             64.3%;  Score 437.5; DB 1;  Length 131;
Best Local Similarity   67.7%;  Pred. No. 2e-29;
Matches  86;  Conservative  12;  Mismatches  28;  Indels  1;  Gaps  1;

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Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
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Db   61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQGNTLPWTFGG 120

Qy  120 GTKLEIK 126
        |||:|||
Db  121 GTKLEIK 127


RESULT 5
US-09-740-002-24
; Sequence 24, Application US/09740002
; Patent No. US2002001798A1
; GENERAL INFORMATION:
;   APPLICANT:  BRAMS, PETER
;   APPLICANT:  MORROW, PHILLIP
;   TITLE OF INVENTION:  NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;   TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;   FILE REFERENCE:  037003-0275759
;   CURRENT APPLICATION NUMBER:  US/09/740,002
;   CURRENT FILING DATE:  2000-12-20
;   PRIOR APPLICATION NUMBER:  09/335,697
;   PRIOR FILING DATE:  1999-06-18
;   PRIOR APPLICATION NUMBER:  08/488,376
;   PRIOR FILING DATE:  1995-06-07
;   NUMBER OF SEQ ID NOS:  27
;   SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH:  234
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
US-09-740-002-24

Query Match             64.0%;  Score 435.5; DB 10;  Length 234;
Best Local Similarity   64.6%;  Pred. No. 5.2e-29;
Matches  82;  Conservative  14;  Mismatches  30;  Indels  1;  Gaps  1;

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Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
         :| |||:  |::: |:||||||   ||||||||:||:|||:||||:||| : |||
Db   61 GKAPKLLIYAGSNLHRGVPSRFSGGGSGTDFTLTINSLQPEDFATYYCQQAYSTPWTFGP 120

Qy  120 GTKLEIK 126
        |||:|||
Db  121 GTKVEIK 127


RESULT 6
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
;   APPLICANT:  SHITARA, KENYA
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;   APPLICANT:  HANAI, NOBUO
;   APPLICANT:  HASEGAWA, MAMORU
;   APPLICANT:  MIYAJI, HIROMASA
;   APPLICANT:  KUWANA, YOSHIHISA
;   TITLE OF INVENTION:  PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;   FILE REFERENCE:  249-101
;   CURRENT APPLICATION NUMBER:  US/09/764,304
;   CURRENT FILING DATE:  2001-01-19
;   EARLIER APPLICATION NUMBER:  09/225,322
;   EARLIER FILING DATE:  1999-01-05
;   EARLIER APPLICATION NUMBER:  US 08/454,680
;   EARLIER FILING DATE:  1995-05-31
;   EARLIER APPLICATION NUMBER:  US 08/408,133
;   EARLIER FILING DATE:  1995-03-21
;   EARLIER APPLICATION NUMBER:  US 08/292,178
;   EARLIER FILING DATE:  1994-08-17
;   EARLIER APPLICATION NUMBER:  US07/947,674
;   EARLIER FILING DATE:  1992-09-17
;   EARLIER APPLICATION NUMBER:  JP 3-238375
;   EARLIER FILING DATE:  1991-09-18
;   NUMBER OF SEQ ID NOS:  19
;   SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH:  128
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  cDNA KM-641
US-09-764-304-10

Query Match             63.9%;  Score 434.5; DB 10;  Length 128;
Best Local Similarity   66.9%;  Pred. No. 3.5e-29;
Matches  85;  Conservative  10;  Mismatches  31;  Indels  1;  Gaps  1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          | | ||||||   | :|||||||  :||||||| :|||:| : ||| |||
Db    1 MMSSAQFLGLLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         :|||||||   |: |||||| ||| |||||||:||:|||:|||| :|| | :  |||||
Db   61 DGTVKLLIFYSSNLHSGVPSRFSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120

Qy  120 GTKLEIK 126
        |||:|||
Db  121 GTKLEIK 127


RESULT 7
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
;   APPLICANT:  SHITARA, KENYA
;   APPLICANT:  HANAI, NOBUO
;   APPLICANT:  HASEGAWA, MAMORU
;   APPLICANT:  MIYAJI, HIROMASA
;   APPLICANT:  KUWANA, YOSHIHISA
;   TITLE OF INVENTION:  PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;   FILE REFERENCE:  249-101
;   CURRENT APPLICATION NUMBER:  US/09/764,304
;   CURRENT FILING DATE:  2001-01-19
;   EARLIER APPLICATION NUMBER:  09/225,322
;   EARLIER FILING DATE:  1999-01-05
;   EARLIER APPLICATION NUMBER:  US 08/454,680
;   EARLIER FILING DATE:  1995-05-31
;   EARLIER APPLICATION NUMBER:  US 08/408,133
;   EARLIER FILING DATE:  1995-03-21
;   EARLIER APPLICATION NUMBER:  US 08/292,178
;   EARLIER FILING DATE:  1994-08-17
;   EARLIER APPLICATION NUMBER:  US07/947,674
;   EARLIER FILING DATE:  1992-09-17
;   EARLIER APPLICATION NUMBER:  JP 3-238375
;   EARLIER FILING DATE:  1991-09-18
```

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match   63.9%; Score 434.5; DB 10; Length 128;
Best Local Similarity   66.9%; Pred. No. 3.5e-29;
Matches   85; Conservative   10; Mismatches   31; Indels   1; Gaps   1;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
            ||||||||| | : ||||||||||: ||| ||| :||::: ||| ||
Db   1 MMSSAQFLGLLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
            :||| :|:| : |||||| ||| | ||||||||||||: | | |||| ||||
Db   61 DGTVKLLIFYSSNLHSGVPSRFSGGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120

Qy   120 GTKLEIK 126
            ||||||
Db   121 GTKLEIK 127

RESULT 8
US-09-229-200A-11
; Sequence 11, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-229-200A-11

Query Match   63.5%; Score 431.5; DB 10; Length 108;
Best Local Similarity   76.4%; Pred. No. 5.2e-29;
Matches   81; Conservative   11; Mismatches   13; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            |||||||||||||||| :||||| ||| | ||| |: ||| | |:|:|| ||||:||

Db   1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYTSTLQPGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
            ||||||||| |||||||||||||||||||| |||| ||||||||
Db   61 RFSGSGSGTDYTFISSLQPEDIATYYCQQYDNLIFTFGQGTKLQI 106

RESULT 9
US-09-229-200A-15
; Sequence 15, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 15
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-229-200A-15

Query Match   63.5%; Score 431.5; DB 10; Length 108;
Best Local Similarity   76.4%; Pred. No. 5.2e-29;
Matches   81; Conservative   11; Mismatches   13; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            |||||||||||| : |:||||| ||| || ||| |: ||| | |:|:|| |||:::||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYTSTLQPGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
            ||||||||| |||||||||||||||||||| |||| ||||||||
Db   61 RFSGSGSGTDYTFISSLQPEDIATYYCQQYDNLIFTFGQGTKLQI 106

RESULT 10
US-09-229-200A-16
; Sequence 16, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA

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;    ZIP: 08933-7003
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;    COMPUTER: IBM
;    OPERATING SYSTEM: PC-DOS
;    SOFTWARE: <Unknown>
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/229,200A
;    FILING DATE: 13-Jan-1999
;    CLASSIFICATION: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;    NAME: John W. Wallen, III
;    REGISTRATION NUMBER: 35,403
;    REFERENCE/DOCKET NUMBER: ORT-948
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (858) 784-3239
;    TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 16
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 108
;    TYPE: amino acid
;    TOPOLOGY: linear
;    SEQUENCE DESCRIPTION: SEQ ID NO: 16
US-09-229-200A-16

Query Match             63.5%;   Score 431.5;  DB 10;   Length 108;
Best Local Similarity   77.4%;   Pred. No. 5.2e-29;
Matches    82; Conservative   10; Mismatches   13; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||:| :|||||| :||||| |:|||||||||||||||||||||||||||
Db    1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYIAWYQHTPGKAPKLLIHYTSTLQPGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
         ||||||| :||:|:|:||||||| ||| :||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYCLQQYDNLIFTFGQGTKLQI 106

RESULT 11
US-09-800-729-150
; Sequence 150, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
;  APPLICANT: Ni et al.
;  TITLE OF INVENTION: 32 Human secreted proteins
;  FILE REFERENCE: P2044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: PCT/US00/26013
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 60/155,709
;  PRIOR FILING DATE: 1999-09-24
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 150
;    LENGTH: 234
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;  FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (120)
;    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150

Query Match             61.8%;   Score 420.5;  DB 10;   Length 234;
Best Local Similarity   63.8%;   Pred. No. 8.7e-28;
Matches    81; Conservative   15; Mismatches   30; Indels   1; Gaps   1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         | |||||||||| || |||||||:||||||||||||:|||||||:|||||||||||||||
Db    1 MRVPAQLLGLLLLWLSGARCDIQLTQSPSSLSASLGDSVTITCQASQDIANYLNWYQQKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
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```
        ||  |:|:|  | ||||| ||| :||||:::|:|||||:|:||| |  :||||::|:||| :|| |||
Db   61 GKRPKLVIFDGSILHTGVPSRFSGGGSGSTHFFTINNLQPDDVATYSCQQYNTFPLTFGX 120

Qy  120 GTKLEIK 126
        |||:|||
Db  121 GTKVEIK 127

RESULT 12
US-09-797-481-2
; Sequence 2, Application US/09797481
; Patent No. US20010047083A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Malaya
;    Kohler, Heinz
;    Foon, Kenneth A.
;    Chatterjee, Sunil K.
;  TITLE OF INVENTION: MURINE ANTI-IDIOTYPE ANTIBODY 3H1
;  NUMBER OF SEQUENCES: 15
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: MORRISON & FOERSTER
;    STREET: 755 Page Mill Road
;    CITY: Palo Alto
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94304-1018
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/797,481
;    FILING DATE: 28-Feb-2001
;    CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 09/361,772
;    FILING DATE: 27-JUL-1999
;    APPLICATION NUMBER: US 08/579,940
;    FILING DATE: 28-DEC-1995
;    APPLICATION NUMBER: US 08/365,484
;    FILING DATE: 28-DEC-1994
;  ATTORNEY/AGENT INFORMATION:
;    NAME: CATHERINE M. POLIZZI
;    REGISTRATION NUMBER: 40,130
;    REFERENCE/DOCKET NUMBER: 304142000102
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (650) 813-5600
;    TELEFAX: (650) 494-0792
;    TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 142 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2

Query Match             61.5%;   Score 418.5;  DB 10;   Length 142;
Best Local Similarity   63.0%;   Pred. No. 7.8e-28;
Matches    80; Conservative   17; Mismatches   29; Indels   1; Gaps   1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         |:||| :||||:|| ||||||:::|||||||||||||| |:||| |:|:|:||| |:||
Db    1 MVSTAQFIGILLLWFPGIKSDIKMTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         | |:: :||| :|:|:| |||||| ||||||||||||||:::|| |||||:||| |||||
Db   61 GKSPKTLIYRANRLIDGVPSRFSGSGSGQVYSLTISSLEYEDMGTYYCLQFDEFPWMFGG 120

Qy  120 GTKLEIK 126
        |||||||
```

```
Db    121 GTKLEIK 127

RESULT 13
US-09-844-736-4
; Sequence 4, Application US/09844736
; Patent No. US2002004187zA1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
;           Foon, Kenneth A.
;           Chatterjee, Sunil K.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
;           CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: MORRISON & FOERSTER
;    STREET: 755 PAGE MILL ROAD
;    CITY: PALO ALTO
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94304-1018
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/844,736
;    FILING DATE: 09-Apr-1997
;    CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/838,692
;    FILING DATE: April 9, 1997
; ATTORNEY/AGENT INFORMATION:
;    NAME: Polizzi, Catherine M.
;    REGISTRATION NUMBER: 40,130
;    REFERENCE/DOCKET NUMBER: 30414-20004.01
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (415) 813-5600
;    TELEFAX: (415) 494-0792
;    TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 142 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-844-736-4

Query Match             61.5%;  Score 418.5;  DB 10;  Length 142;
Best Local Similarity   63.0%;  Pred. No. 7.8e-28;
Matches   80;  Conservative  17;  Mismatches  29;  Indels  1;  Gaps  1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          | :||||||:|| | :|:||||||||| |||| :||||| |:  ||| | :|
Db    1 MVSTAQFLGILLLWFPGIKSDIKMTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGG 119
          |  :|: ||: : |:||||||||| |||| |||:||||| |:  | | :||
Db   61 GKSPKTLIYRANRLIDGVPSRFSGSGSGSGQVYSLTISSLEYEDMCTYCLQFDEFPWMFGG 120

Qy  120 GTKLEIK 126
          |||||||
Db  121 GTKLEIK 127

RESULT 14
US-09-740-002-26
; Sequence 26, Application US/09740002
; Patent No. US2002001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
```

```
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 26
;    LENGTH: 234
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-740-002-26

Query Match             61.2%;  Score 416;  DB 10;  Length 234;
Best Local Similarity   63.5%;  Pred. No. 2e-27;
Matches   80;  Conservative  16;  Mismatches  30;  Indels  0;  Gaps  0;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          || | |||||| ||  :|:||||||||||||||:| :||||| |:: |||| |
Db    3 MRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSIASYVNWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          |  |:||| |: | :||||||||||||| ||||:|||| |: :|: |||| :  | :|
Db   63 GKAPKVLIFASANLVSGVPSRFSGSGSGTVFTLTISNLQPEDFATYFCQQSYTNFSFGQG 122

Qy  121 TKLEIK 126
          ||||||
Db  123 TKLEIK 128

RESULT 15
US-09-855-271-26
; Sequence 26, Application US/09855271
; Patent No. US2002004208A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 26
;    LENGTH: 128
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US2002004208A1e1 Sequence
US-09-855-271-26

Query Match             61.0%;  Score 414.5;  DB 10;  Length 128;
Best Local Similarity   65.6%;  Pred. No. 1.5e-27;
Matches   80;  Conservative  16;  Mismatches  25;  Indels  1;  Gaps  1;

Qy    6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
          | |||||| |:||||| |||||||||||||||:||:|| | ||| | ||:| | :|
Db    6 QVLGLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCLASEGISSYLAWYQQKPGKAPK 65

Qy   66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
          |||: || | :|||||||| |||| |||:||||  |:  |||| |:: | :|
Db   66 LLIYGANSLQTGVPSRFSGSGSGSATDYTLTISSLQPEDFATYYCQQSYKFPNTFGQGTKVE 125

Qy  125 IK 126
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us-09-155-739-2.rapb

Mon Jan 6 14:19:34 2003

Db   126 VK 127

Search completed: January 6, 2003, 13:29:30
Job time : 7.10909 secs

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                GenCore version 5.1.3
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    January 6, 2003, 13:12:26 ; Search time 11.7091 Seconds
                                      (without alignments)
                                      1034.490 Million cell updates/sec

Title:      US-09-155-739-2
Perfect score:  680
Sequence:   1 MRPSIQFIGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:   283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_73:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	589	86.6	125	2	S09365	Ig kappa chain - m
2	535	78.7	104	2	S26330	Ig kappa chain V r
3	526	77.4	104	2	S26329	Ig kappa chain V r
4	524	77.1	106	2	C33936	Ig kappa chain V r
5	490.5	72.1	129	2	S52789	Ig kappa chain V r
6	490	72.1	103	2	S26332	Ig kappa chain V r
7	488	71.8	97	2	PH1064	Ig light chain V r
8	476	70.0	94	2	E33730	Ig kappa chain V r
9	471.5	69.3	107	2	PL0270	Ig kappa chain V r
10	465.5	68.5	107	2	PL0272	Ig kappa chain V r
11	464.5	68.3	107	2	PL0269	Ig kappa chain V r
12	464.5	68.3	107	2	PL0271	Ig kappa chain V r
13	453.5	66.7	127	2	S40367	Ig kappa chain V-J
14	445.5	65.5	132	2	S40334	Ig kappa chain - h
15	445.5	65.4	139	2	S40365	Ig kappa chain - h
16	443.5	65.2	129	2	S40317	Ig kappa chain V-J
17	442.5	65.1	125	2	S40333	Ig kappa chain V-J
18	442.5	65.1	131	2	S40352	Ig kappa chain pre
19	441.5	64.9	129	1	K1HUWK	Ig kappa chain V r
20	439.5	64.6	94	2	PH1063	Ig light chain V r
21	439	64.6	124	2	S40336	Ig kappa chain V-J
22	438.5	64.5	123	2	S40331	Ig kappa chain - h
23	438	64.4	117	2	S42263	Ig kappa chain V r
24	437.5	64.3	122	2	A29380	Ig kappa chain pre
25	437.5	64.3	127	2	S52447	Ig kappa chain V r
26	437.5	64.3	135	2	S24320	Ig kappa chain pre
27	437.5	64.3	128	2	PL0101	Ig kappa chain pre
28	436.5	64.2	129	2	S52793	Ig kappa chain V r
29	435.5	64.0	127	2	S04574	Ig kappa chain pre
30	435.5	64.0	127	2	S11240	Ig kappa chain V r
31	434.5	63.9	141	2	A49134	Ig kappa chain V-I
32	433.5	63.7	126	2	A34904	Ig kappa chain pre
33	433.5	63.7	234	2	S14237	Ig kappa chain V r
34	432	63.5	117	2	S43528	Ig kappa chain pre
35	430.5	63.5	127	2	PH1224	Ig kappa chain - h
36	428.5	63.0	125	2	S40316	Ig kappa chain V r
37	427.5	62.7	129	2	S52792	Ig kappa chain V r
38	426.5	62.7	125	2	S40350	Ig kappa chain - h
39	425.5	62.6	125	2	S40349	Ig kappa chain V-J
40	425.5	62.6	128	1	KVMST1	Ig kappa chain pre
41	422.5	62.1	124	2	S40348	Ig kappa chain V-J
42	419.5	61.7	122	2	S40314	Ig kappa chain - h
43	419.5	61.7	124	2	S03521	Ig kappa chain pre
44	418	61.5	127	2	A23986	Ig kappa chain V r
45	416.5	61.3	85	2	F36025	Ig light chain V r

ALIGNMENTS

```
RESULT 1
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene s
A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match      86.6%;    Score 589;  DB 2;   Length 125;
Best Local Similarity   90.6%;   Pred. No. 5.9e-44;
Matches 115;   Conservative 2;   Mismatches 6;   Indels 4;   Gaps 2;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         |||||||||||||||||||   :||||||||||||||||||||::||||||:||||||||
Db   1 MRPSIQFLGLLLFWLHG---DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 57

Qy  61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW-TFGG 119
         || |||||||||| |||||||||||||| |||| :||| |||||||||||||||  ||||
Db  58 GKGPRLLIHYTSTLQPGIPSRFSGSGSGDYSFSISNLGPEDIATYYCLQYDNLLRTFGG 117

Qy 120 GTKLEIK 126
         |||||||
Db 118 GTKLEIK 124

RESULT 2
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
```

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   78.7%;   Score 535; DB 2;   Length 104;
Best Local Similarity 95.2%;   Pred. No. 2.2e-39;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||||||||| |||||:|||||||||||||| |||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
         ||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 3
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.4%;   Score 526; DB 2;   Length 104;
Best Local Similarity 94.2%;   Pred. No. 1.3e-38;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||||||||| |||||:|||||||||||||| |||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
         ||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 4
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4464-4468, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.1%;   Score 524; DB 2;   Length 106;
Best Local Similarity 91.5%;   Pred. No. 2e-38;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||||||||| |||||:||||| |||||||||| |||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIALWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
         ||||||||||||||||||:|:|||::|||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLDPEIATYYCLQYDSLYTFGGGTKLEIK 106

RESULT 5
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelo
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   72.1%;   Score 490.5; DB 2;   Length 129;
Best Local Similarity 72.4%;   Pred. No. 1.9e-35;
Matches 92; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          : ::|:::|:| ::: ||||||||||||||||||||: |||||:|||||||||
Db   3 MRVPAQLLGLLLLWLSGARCDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         |:|| |||| :|::|| :| |||||||||||| ||:|||||||:| :||||||| ||||
Db   63 GKAPKLLIHAASSLETGVPSRFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGG 122

Qy   120 GTKLEIK 126
         |||:|||
Db   123 GTKVEIK 129

RESULT 6
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332, S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   72.1%;   Score 490; DB 2;   Length 103;
Best Local Similarity 87.4%;   Pred. No. 1.6e-35;
Matches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||||||||||||| || | :||||||||||| :|||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKGPRLLIHYTSTLQPGIPS 80

Db   1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLLIMDYTSSLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKL 123
         ||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103

RESULT 7
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x N2W]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   71.8%;   Score 488; DB 2;   Length 97;
Best Local Similarity   93.8%;   Pred. No. 2.3e-35;
Matches   91; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||||||||||||||| ||||||| |||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTF 117
         |||||||||||||||||||||||||||||||||| ||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97

RESULT 8
E33730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
A;Accession: E33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   70.0%;   Score 476; DB 2;   Length 94;
Best Local Similarity   94.7%;   Pred. No. 2.4e-34;
Matches   89; Conservative   2; Mismatches   2; Indels   3; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||||||||||||| ||||||| |||||||||||||||||| |||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL 114
         ||||||||||||||| ||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94

RESULT 9
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   69.3%;   Score 471.5; DB 2;   Length 107;
Best Local Similarity   86.0%;   Pred. No. 6.7e-34;
Matches   92; Conservative   5; Mismatches   9; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||||| |||||| ||||||||||| || |||| ||||||||||||||||
Db   1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         ||||||||||||||| ||||||||||||||||| : :|| |||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   68.5%;   Score 465.5; DB 2;   Length 107;
Best Local Similarity   85.0%;   Pred. No. 2.2e-33;
Matches   91; Conservative   5; Mismatches   10; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||||| |||||| ||||||||||| || |||| ||||||||||||||||
Db   1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         ||||||||||||||| ||||||||||||||||| : :|| |||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 11

PL0269
Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:9011618; PMID:2104919
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   68.3%; Score 464.5; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 2.7e-33;
Matches   91; Conservative   4; Mismatches   11; Indels   1; Gaps   1;

Qy 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||| |||||||| |||:|||| |||||| :|| |||||||||||||||||
Db   1 DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNMAWYQHKAGKPRLLIWYTSTLQPGIPS 60

Qy 81 RFSGSGSGRDYSFSNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
        |||||||||||| ::|||||||||||| :||| ::||||||||||
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 12
PL0271
Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:9011618; PMID:2104919
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   68.3%; Score 464.5; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 2.7e-33;
Matches   91; Conservative   4; Mismatches   11; Indels   1; Gaps   1;

Qy 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        ||||||||||||| |||||| |||:|||| |||||| :|| |||||||||||||||||
Db   1 DIQMTQPCSLSASLGDKVITFCRTSQDIRKNMAWYQHKACKGPRLLIWYTSTLQPGIPS 60

Qy 81 RFSGSGSGRDYSFSNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
        |||||||||||| :|||||||||||| :||| ::||||||||||
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 13
S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match   66.7%; Score 453.5; DB 2; Length 127;
Best Local Similarity 68.9%; Pred. No. 2.8e-32;
Matches   84; Conservative   16; Mismatches   21; Indels   1; Gaps   1;

Qy   6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
        | |||||| ||:|||::|||||||||||||||| : ||||| |: |||||||||||||||
Db   3 QLLGLLLWLRLGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPK 62

Qy 66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
        |||| :||||||| |||||||||||| ::|: ||||||||||| :|||: ||||||||
Db 63 LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAYYCQQSYNTPWTFGQGTKVE 122

Qy 125 IK 126
        ||
Db 123 IK 124

RESULT 14
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match   65.5%; Score 445.5; DB 2; Length 132;
Best Local Similarity 64.6%; Pred. No. 1.4e-31;
Matches   82; Conservative   21; Mismatches   23; Indels   1; Gaps   1;

Qy   1 MRPSIQFIGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
        ||| |: ||| | || | |||:|||||||||||||||| : ||||| |: |||||||| |
Db   2 MRVPAQLLGLLLWLPGARCDIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKP 61

Qy 61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
        ||:| |||| :|||||||| :|: ||||||||| ::|: ||||||||||| :||| ||
Db 62 GKAPKLLIYVASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGG 121

Qy 120 GTKLEIK 126
        ||||:||
Db 122 GTKVEIR 128

RESULT 15

S40365
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40365
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match   65.4%; Score 444.5; DB 2; Length 139;
Best Local Similarity   68.9%; Pred. No. 1.8e-31;
Matches   84; Conservative   14; Mismatches   23; Indels   1; Gaps   1;

Qy   6 QFLGILLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
            : |||| || | || ||||||||||||||: : :||||: :|| : ||||||| |
Db   1 QLLGILLLWLSGATCDIQMTQSPSSLSASVGDRVTITCQATQDIGNYLNWYQHKPGKAPN 60

Qy   66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE 124
            |||: : |: |:||||| || ::| ||:::||||||||||:|| || :||| |||:
Db   61 LLIYDASNLETGVPSRFSGRGSGTHFTFTISSLQPEDIATYYCCQYGNLPFTFGPGTKVH 120

Qy   125 IK 126
           ||
Db   121 IK 122

Search completed: January 6, 2003, 13:18:18
Job time : 12.7091 secs

```
                GenCore version 5.1.3
        Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    January  6, 2003, 12:48:25 ; Search time 6.36364 Seconds
                                         (without alignments)
                                         821.231 Million cell updates/sec

Title:          US-09-155-739-2
Perfect score:  680
Sequence:       1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:    112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	441.5	64.9	129	1	KV1W_HUMAN	P04431 homo sapien
2	425.5	62.6	128	1	KV5E_MOUSE	P01637 mus musculu
3	412.5	60.7	129	1	KV1X_HUMAN	P04432 homo sapien
4	402	59.1	117	1	KV1J_HUMAN	P01602 homo sapien
5	400	58.8	115	1	KV5F_MOUSE	P01638 mus musculu
6	397.5	58.5	108	1	KV1B_HUMAN	P01594 homo sapien
7	395.5	58.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	392.5	57.7	108	1	KV1P_HUMAN	P01608 homo sapien
9	389.5	57.3	108	1	KV1Y_HUMAN	P80362 homo sapien
10	380.5	56.0	108	1	KV1A_HUMAN	P01593 homo sapien
11	379.5	55.8	108	1	KV1M_HUMAN	P01605 homo sapien
12	378.5	55.7	130	1	KV5G_MOUSE	P01639 mus musculu
13	378.5	55.7	133	1	KV4B_HUMAN	P06313 homo sapien
14	378	55.6	117	1	KV1I_HUMAN	P01601 homo sapien
15	377.5	55.5	108	1	KV5J_MOUSE	P01643 mus musculu
16	377	55.4	107	1	KV1D_HUMAN	P01596 homo sapien
17	375	55.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	374.5	55.1	108	1	KV5O_MOUSE	P01648 mus musculu
19	373.5	54.9	108	1	KV1Q_HUMAN	P01609 homo sapien
20	373.5	54.9	108	1	KV5N_MOUSE	P01647 mus musculu
21	371.5	54.6	108	1	KV5K_MOUSE	P01644 mus musculu
22	369.5	54.3	108	1	KV5M_MOUSE	P01646 mus musculu
23	368.5	54.2	108	1	KV5L_MOUSE	P01645 mus musculu
24	366.5	53.9	108	1	KV1R_HUMAN	P01610 homo sapien
25	362.5	53.3	108	1	KV1C_HUMAN	P01595 homo sapien
26	360.5	53.0	108	1	KV1H_HUMAN	P01600 homo sapien
27	359.5	52.9	108	1	KV1N_HUMAN	P01606 homo sapien
28	357.5	52.6	108	1	KV1E_HUMAN	P01597 homo sapien
29	357.5	52.6	108	1	KV1V_HUMAN	P04430 homo sapien
30	355.5	52.3	108	1	KV1F_HUMAN	P01598 homo sapien
31	354.5	52.1	108	1	KV1S_HUMAN	P01611 homo sapien
32	353.5	52.0	115	1	KV5C_MOUSE	P01635 mus musculu
33	352.5	51.8	108	1	KV1K_HUMAN	P01603 homo sapien
34	350.5	51.5	108	1	KV1L_HUMAN	P01604 homo sapien
35	349.5	51.4	108	1	KV5U_MOUSE	P04946 mus musculu
36	347	51.0	129	1	KV3H_HUMAN	P04207 homo sapien
37	347	51.0	129	1	KV3M_HUMAN	P18136 homo sapien
38	343	50.4	117	1	KV5H_MOUSE	P01641 mus musculu
39	341.5	50.2	108	1	KV1G_HUMAN	P01599 homo sapien
40	341	50.1	110	1	KV3P_MOUSE	P01668 mus musculu
41	339.5	49.9	108	1	KV5T_MOUSE	P01653 mus musculu
42	338	49.7	129	1	KV3L_HUMAN	P18135 homo sapien
43	337.5	49.6	131	1	KV3I_MOUSE	P01661 mus musculu
44	335.5	49.3	108	1	KV5P_MOUSE	P01649 mus musculu
45	335.5	49.3	108	1	KV5Q_MOUSE	P01650 mus musculu

ALIGNMENTS

```
RESULT 1
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;     PRT;    129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; KIHUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE  129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

Query Match        64.9%;    Score 441.5;  DB 1;  Length 129;
Best Local Similarity   66.9%;    Pred. No. 2.6e-38;
Matches   85;  Conservative   15;  Mismatches  26;  Indels   1;  Gaps   1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
Db    3 MRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP 62
```

```
Qy    61  GKRPLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
          || :|:||: :|| : |||||||| :|| :|| ||||||| |: ||||| || :| |||
Db    63  GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122

Qy   120  GTKLEIK 126
          ||:|||
Db   123  GTRLEIK 129

RESULT 2
KV5E_MOUSE
ID   KV5E_MOUSE    STANDARD;          PRT;    128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region T1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; V00772; CAA24150.1; -.
DR   PIR; A01920; KVMST1.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION T1.
FT   DOMAIN       21     43       FRAMEWORK-1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    108       FRAMEWORK-3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      118    127       FRAMEWORK-4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE  128 AA;  14385 MW;  AFA5563D31BB7E05 CRC64;

Query Match             62.6%;  Score 425.5;  DB 1;  Length 128;
Best Local Similarity   62.2%;  Pred. No. 1.1e-36;
Matches   79;  Conservative 18;  Mismatches  29;  Indels  1;  Gaps  1;

Qy     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          || |||||:||||||: ||||| |:|||||||: ||| :| ::|:| :|||| :|:: ||
Db     1  MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKP 60

Qy    61  GKRPLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
          || :| :|:  ||:| |||||||||||: :| ||::||  |: |:||||| |  | ||
Db    61  GKSPKTLLYRANRLVDGVPSRFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGA 120

Qy   120  GTKLEIK 126
          ||||:|
Db   121  GTKLELK 127

RESULT 3
KV1X_HUMAN
ID   KV1X_HUMAN    STANDARD;          PRT;    129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Daudi precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
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CC   -----------------------------------------------------------------------
DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; KIHUDI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE  129 AA;  14235 MW;  CAF076BC7E5574C8 CRC64;

Query Match             60.78%;  Score 412.5;  DB 1;  Length 129;
Best Local Similarity   61.4%;  Pred. No. 2.4e-35;
Matches   78;  Conservative 19;  Mismatches  29;  Indels  1;

Qy     1  MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          || :||||||||||||||||||||||||||||||: | :|||| : :|:|| :| :: ||
Db     3  MRVPAQLGLLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKP 62

Qy    61  GKRPLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
          || : |||| :|||: :|||||||||| :: :::::||||| ||||||:| |: : ||||
Db    63  GKAPTLLIYAVSNLQVGVPSRFSGSGSGAEFTLTISSLQPEDFATYYCQQYNFSFTFGG 122

Qy   120  GTKLEIK 126
          ||:: |:
Db   123  GTKVDNK 129

RESULT 4
KV1J_HUMAN
ID   KV1J_HUMAN    STANDARD;          PRT;    117 AA.
AC   P01602;
```

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DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region HK102 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
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CC   --------------------------------------------------------------------------
DR   EMBL; J00245; AAA59087.1; -.
DR   EMBL; Z00001; CAA77292.1; -.
DR   PIR; A01882; K1HU12.
DR   HSSP; P01607; 1REI.
DR   Genew; HGNC:5741; IGKV1-5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     22
FT   CHAIN         23   >117       IG KAPPA CHAIN V-I REGION HK102.
FT   DOMAIN        23    45        FRAMEWORK-1.
FT   DOMAIN        46    56        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        57    71        FRAMEWORK-2.
FT   DOMAIN        72    78        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        79   110        FRAMEWORK-3.
FT   DOMAIN       111   >117       COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID      45   110        BY SIMILARITY.
FT   NON_TER      117   117
SQ   SEQUENCE   117 AA;  12768 MW;  AD1DF3A40AF1A49B CRC64;

Query Match             59.18%;  Score 402;  DB 1;  Length 117;
Best Local Similarity   63.7%;  Pred. No. 2.5e-34;
Matches   72;  Conservative   21;  Mismatches   20;  Indels   0;  Gaps   0;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
        | | |||||| || ||||||||||||||||  :|||||   : ::|||| || ||||
Db    3 MRVPAQLGLLLLWLPGAKCDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
        || |:||| :  |: ||||||| |:||||||  ::|: :| ||||||||||::
Db   63 GKAPKLLIYDASSLESGVPSRFSGSGSGGTEFTLTISSLQPDDFATYYCQQYNS 115

RESULT 5
KV5F_MOUSE
ID   KV5F_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region L6 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     20
FT   CHAIN         21   >115       IG KAPPA CHAIN V-V REGION L6.
FT   DOMAIN        21    43        FRAMEWORK-1.
FT   DOMAIN        44    54        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        55    69        FRAMEWORK-2.
FT   DOMAIN        70    76        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        77   108        FRAMEWORK-3.
FT   DOMAIN       109   >115       COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID      43   108        BY SIMILARITY.
FT   NON_TER      115   115
SQ   SEQUENCE   115 AA;  12986 MW;  BA852C58F328E1C3 CRC64;

Query Match             58.8%;  Score 400;  DB 1;  Length 115;
Best Local Similarity   65.2%;  Pred. No. 4e-34;
Matches   73;  Conservative   15;  Mismatches   24;  Indels   0;  Gaps   0;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
        |||||| |:|||||||||| |  :|||:|||||  |||| |||||||||||:|||  ||| ||
Db    1 MRTPAQFLGLLLWFPGIKCDIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYD 112
        || || ||  : :  ||||||||||||| :|||||||| |:|| :| |||||
Db   61 GKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYD 112

RESULT 6
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; K1HUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23        FRAMEWORK-1.
FT   DOMAIN       24     34        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49        FRAMEWORK-2.
FT   DOMAIN       50     56        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88        FRAMEWORK-3.
FT   DOMAIN       89     97        COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107        FRAMEWORK-4.
FT   DISULFID     23     88        BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

Query Match             58.5%;  Score 397.5;  DB 1;  Length 108;
Best Local Similarity   70.1%;  Pred. No. 6.7e-34;
Matches   75;  Conservative   14;  Mismatches   17;  Indels    1;  Gaps    1;

Qy         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
              |||||||||||||: :||||| :|||||: ||| ||| :|| :|||:| :|:||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
              |||||||||  ::|:|||||||::||||||||: |||:||||||: |:||
Db         61 RFSGSGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
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RESULT 7

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ID   KV1O_HUMAN    STANDARD;     PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei): isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; K1HURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23        FRAMEWORK-1.
FT   DOMAIN       24     34        COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49        FRAMEWORK-2.
FT   DOMAIN       50     56        COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88        FRAMEWORK-3.
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FT   DOMAIN       89     97        COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107        FRAMEWORK-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

Query Match             58.2%;  Score 395.5;  DB 1;  Length 108;
Best Local Similarity   71.7%;  Pred. No. 1.1e-33;
Matches   76;  Conservative   13;  Mismatches   16;  Indels    1;  Gaps    1;

Qy         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
              |||||||||||||: :||||| :|||| ||| ||| :|| :|||:| :|:||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
              ||||||||| ::|:|||||||::|||||| :|| |||:||||||: :|
Db         61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPVTFGQGTKLQI 106
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RESULT 8

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ID   KV1P_HUMAN    STANDARD;     PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; K1HURY.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
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KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23     88      BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11782 MW;  F5ACEDE5A313DF3A CRC64;

Query Match                   57.7%;    Score 392.5;   DB 1;  Length 108;
Best Local Similarity          68.2%;   Pred. No. 2.2e-33;
Matches   73;  Conservative   18;  Mismatches   15;  Indels   1;  Gaps     1;

Qy    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          ||||||||||||| :|| ::||||| :|::|| :: ||: |: |: |:||
Db     1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
          |||| |:::|  ||:|:|::|||:||||||||| |:|| |||||||::|
Db    61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107

RESULT 9
KV1Y_HUMAN
ID   KV1Y_HUMAN          STANDARD;        PRT;    108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
RN   [2]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23     88      BY SIMILARITY.
FT   CONFLICT     30     31      TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11737 MW;  D9D941B3F0FAE697 CRC64;
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Query Match                   57.3%;    Score 389.5;   DB 1;  Length 108;
Best Local Similarity          67.3%;   Pred. No. 4.4e-33;
Matches   72;  Conservative   18;  Mismatches   16;  Indels   1;  Gaps     1;

Qy    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          ||||||||||||| :|| ::||||| :|::|| :|:: :||:|| :||: |: |:||
Db     1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
          |||||| ||:|:|::|::|||:||||||||| |:|:| |||||||
Db    61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107

RESULT 10
KV1A_HUMAN
ID   KV1A_HUMAN          STANDARD;        PRT;    108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; KIHUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107      FRAMEWORK-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11992 MW;  E3B3B246C18F0C4F CRC64;

Query Match                   56.0%;    Score 380.5;   DB 1;  Length 108;
Best Local Similarity          69.2%;   Pred. No. 3.7e-32;
Matches   74;  Conservative   12;  Mismatches   20;  Indels   1;  Gaps     1;

Qy    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          ||||||||||||| :|| ::||||| :|::||  :|: :|| ::|: |: |:||
Db     1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60

Qy    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
          |||||| ||:|:|::|::|||:||||||||| |:|:| |||||||
Db    61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGGGTKLEIK 107

RESULT 11
KV1M_HUMAN
ID   KV1M_HUMAN          STANDARD;        PRT;    108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

Query Match             55.8%;  Score 379.5;  DB 1;  Length 108;
Best Local Similarity   65.7%;  Pred. No. 4.6e-32;
Matches   71;  Conservative   17;  Mismatches   17;  Indels    3;  Gaps    2;

Qy         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
              |||||||||||| |:||||| ||| ||| |:|||| :|:| |:|
Db          1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
              |||||||| |:|:||||||||:|||||||||  |:|  ||| |||||:|
Db         61 RFSGSGSGTDFTTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK 107


RESULT 12
KV5G_MOUSE
ID   KV5G_MOUSE     STANDARD;      PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-v region MOPC 41 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa-immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambdal-type and kappa-type light
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RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.;
RT   "Mechanism of antibody synthesis: size differences between mouse
RT   kappa chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC       SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal; Bence-Jones protein.
FT   SIGNAL        1     22
FT   CHAIN        23    130       IG KAPPA CHAIN V-V REGION MOPC 41.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   VARIANT       1      2       MISSING (IN 25% OF THE MOLECULES).
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14311 MW;  5EF0FE71D5F1BEC CRC64;

Query Match             55.7%;  Score 378.5;  DB 1;  Length 130;
Best Local Similarity   59.1%;  Pred. No. 7.2e-32;
Matches   75;  Conservative   13;  Mismatches   38;  Indels    1;  Gaps    1;

Qy          1 MRPSIQFLGILLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
              ||  : ||| | ||||||||||||||||||||| |||:||
Db          3 MRAPAQIFGFLLLLFQGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP 62

Qy         61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
              ||  |||| ||| |:||||| ||||||:|||||||||| :  ||||| ||||
Db         63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG 122

Qy        120 GTKLEIK 126
              |||||||
Db        123 GTKLEIK 129


RESULT 13
KV4B_HUMAN
ID   KV4B_HUMAN     STANDARD;      PRT;   133 AA.
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region JI precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041853; PubMed=2997712;
RA   Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
-------------------------------------------------------------------
DR   EMBL; Z00022; CAA77317.1; -.
DR   PIR; A01904; K4HUJI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    133       IG KAPPA CHAIN V-IV REGION JI.
FT   DOMAIN       21    133       FRAMEWORK-1.
FT   DOMAIN       43     43       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       44     60       FRAMEWORK-2.
FT   DOMAIN       61     75       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       76     82       FRAMEWORK-3.
FT   DOMAIN       83    114       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      115    122       FRAMEWORK-4.
FT   DOMAIN      123    132       BY SIMILARITY.
FT   DISULFID     43    114
FT   NON_TER     133    133
SQ   SEQUENCE    133 AA;   14632 MW;  5FB3953066744AF4 CRC64;

Query Match       55.7%;   Score 378.5;   DB 1;   Length 133;
Best Local Similarity   57.9%;   Pred. No. 7.4e-32;
Matches   73;   Conservative  20;   Mismatches  26;   Indels   7;   Gaps   3;

Qy      7 FLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI----NK-YMAWYQHKP 60
            |:|||| || ||:|||:||  || ||||||||||||||||||    || |:||||||||
Db      8 FISLLL-WISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKP 66

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
            |:||||:: :|:|  ||||||||| ||:| |||| || |||| ||||
Db     67 GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIPTFGGG 126

Qy    121 TKLEIK 126
            |:|||
Db    127 TKVEIK 132


RESULT 14
KV1I_HUMAN
ID   KV1I_HUMAN      STANDARD;      PRT;    117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region HK101 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83129397; PubMed=6402305;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin V genes: evidence indicating that
RT   recently duplicated human v kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
CC   -------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; K01322; AAA58930.1; -.
DR   EMBL; K01324; AAA58932.1; -.
DR   EMBL; V00558; CAA23824.1; -.
DR   PIR; A01881; K1HU11.
DR   PIR; A21056; A21056.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    >117      IG KAPPA CHAIN V-I REGION HK101.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    >117      COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;   12799 MW;  D7D0FF3718CEF587 CRC64;

Query Match       55.6%;   Score 378;   DB 1;   Length 117;
Best Local Similarity   62.8%;   Pred. No. 7.2e-32;
Matches   71;   Conservative  17;   Mismatches  25;   Indels   0;   Gaps   0;

Qy      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
            ||  |||||  |||||||||||||||||||||||||||||| : |:||:|||:|||||||
Db      3 MRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP 62

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
            |:||  |||| |||||  :||||||||||| || |:|| |||||| ||||::
Db     63 EKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNS 115


RESULT 15
KV5J_MOUSE
ID   KV5J_MOUSE      STANDARD;      PRT;    108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01926; KVMS73.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; IGv; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
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FT   DOMAIN          50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN          57     88       FRAMEWORK-3.
FT   DOMAIN          89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN          98    108       FRAMEWORK-4.
FT   DISULFID        23     88       BY SIMILARITY.
FT   NON_TER        108    108
SQ   SEQUENCE       108 AA;   11819 MW;  2AD29D92A72AA0A3 CRC64;

Query Match           55.5%;   Score 377.5;  DB 1;  Length 108;
Best Local Similarity 67.3%;   Pred. No. 7.4e-32;
Matches    72;  Conservative   12;  Mismatches   22;   Indels    1;  Gaps    1;

Qy     21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
               ||||||: |||||||| :|||:| || | |: ||| ||    :|||:|||:| |:|
Db      1  DIQMTQTTSSLSASLGDRVTISCCSASQSIGNYLBWYQQKPDGTVKLLIYTSSLHSGVPS  60

Qy     81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
               ||||||| ||| :||:|:||||||| |  :| | |||||||||||
Db      61  RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIK 107


Search completed: January  6, 2003, 13:15:45
Job time : 6.36364 secs
```

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 6, 2003, 13:10:51 ; Search time 23.6727 Seconds
                                     (without alignments)
                                     1096.702 Million cell updates/sec

Title: US-09-155-739-2
perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC..........YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   SPTREMBL_21:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	468	68.8	241	11	Q921A6	Q921a6 mus musculu
2	424.5	62.4	234	11	Q8R062	Q8r062 mus musculu
3	412.5	60.7	233	11	Q91WS9	Q91ws9 mus musculu
4	410.5	60.4	234	11	Q91WF8	Q91wf8 mus musculu
5	389.5	57.3	108	4	Q9UL77	Q9ul77 homo sapien
6	387	56.9	107	4	Q96SA9	Q96sa9 homo sapien
7	380.5	56.0	214	11	Q9R1A5	Q9r1a5 mus musculu
8	378.5	55.7	108	4	Q9UL70	Q9ul70 homo sapien
9	374.5	55.1	234	11	Q8VCP0	Q8vcp0 homo sapien
10	372.5	54.8	107	11	Q9JL84	Q9jl84 mus musculu
11	367.5	54.0	127	4	Q92SS9	Q92ss9 mus musculu
12	362	53.2	107	4	Q9UL81	Q9ul81 homo sapien
13	354.5	52.1	109	11	Q920E6	Q920e6 mus musculu
14	346.5	51.0	108	4	Q9UL79	Q9ul79 homo sapien
15	341.5	50.2	298	11	Q9QYF0	Q9qyf0 mus musculu
16	332.5	48.9	116	4	Q96PF6	Q96pf6 homo sapien
17	327.5	48.2	234	11	Q8R028	Q8r028 mus musculu
18	319.5	47.0	111	11	Q920E9	Q920e9 mus musculu
19	319	46.9	109	4	Q9UL78	Q9ul78 homo sapien
20	318	46.8	239	4	Q8TCD0	Q8tcd0 homo sapien
21	317.5	46.7	238	11	Q99M37	Q99m37 mus musculu
22	316	46.5	134	11	Q8VDD0	Q8vdd0 mus musculu
23	311.5	45.8	108	11	Q8VIJ0	Q8vij0 mus musculu
24	310	45.6	109	4	Q9UL85	Q9ul85 homo sapien
25	308.5	45.4	238	11	Q8VCI6	Q8vci6 mus musculu
26	308	45.3	109	4	Q9UL86	Q9ul86 homo sapien
27	305.5	44.9	108	4	Q9UL83	Q9ul83 homo sapien
28	299	44.0	106	5	Q9U410	Q9u410 schistosoma
29	295.5	43.5	107	11	Q9ER29	Q9erz9 mus musculu
30	295	43.4	239	11	Q8VC55	Q8vc55 mus musculu
31	292.5	43.0	101	11	Q9JL78	Q9jl78 mus musculu
32	291.5	42.9	97	11	Q9JL76	Q9jl76 mus musculu
33	289.5	42.6	103	11	Q9JL80	Q9jl80 mus musculu
34	288.5	42.4	99	11	Q9JL74	Q9jl74 mus musculu
35	283	41.6	235	11	Q91W12	Q91w12 mus musculu
36	281.5	41.4	114	4	Q9UL80	Q9ul80 homo sapien
37	262	38.5	104	11	Q9JL82	Q9jl82 mus musculu
38	252.5	37.1	109	6	Q9N0W5	Q9n0w5 oryctolagus
39	228	33.5	233	4	Q8TBC9	Q8tbc9 homo sapien
40	214	31.5	110	4	Q8TE63	Q8te63 homo sapien
41	211.5	31.1	237	4	Q8WUK4	Q8wuk4 homo sapien
42	210	30.9	240	4	Q8WUK3	Q8wuk3 homo sapien
43	209	30.7	107	4	Q9NSD6	Q9nsd6 homo sapien
44	208.5	30.7	237	4	Q8WTU6	Q8wtu6 homo sapien
45	204.5	30.1	107	4	Q9UL82	Q9ul82 homo sapien

ALIGNMENTS

RESULT 1
Q921A6
ID   Q921A6;   PRELIMINARY;   PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Anti-CEA 79 single chain Fv fragment (fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
DR   EMBL; U88067; AAB48044.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
FT   NON_TER   1
FT   NON_TER   241
SQ   SEQUENCE   241 AA; 26086 MW; 027688724B9C771 CRC64;

Query Match   68.8%; Score 468; DB 11; Length 241;
Best Local Similarity   80.9%; Pred. No. 8e-44;
Matches   89; Conservative   6; Mismatches   15; Indels   0; Gaps   0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          ||::||||||||||||||||||||||||||||||||||||||||||| || :||
Db   130 GGGSDIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSAHTLHIYIQP 189

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||||||||||||||||||||| ||||||||||:|
Db   190 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLHTFGGGTKLELK 239

```
RESULT 2
Q8R062
ID   Q8R062        PRELIMINARY;       PRT;   234 AA.
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25857 MW;  4EB08C81426AEAB1 CRC64;

Query Match             62.4%;  Score 424.5;  DB 11;  Length 234;
Best Local Similarity   66.1%;  Pred. No. 5.2e-39;
Matches   84;  Conservative  11;  Mismatches  31;  Indels  1;  Gaps  1;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         : ||||||| |:|||||||| :||||||||||||||  : |: || || ||||| ||
Db   1 MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKP 60

Qy  61 GKRPLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         :||:||:|: :||:|||||||||||||  ||||||| |||||||||||:  :  :|||
Db  61 DGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGS 120

Qy 120 GTKLEIK 126
         ||||||
Db 121 GTKLEIK 127

RESULT 3
Q91WS9
ID   Q91WS9        PRELIMINARY;       PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 25.8 kDa protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   233 AA;  25781 MW;  B1C184DA149A16EB CRC64;

Query Match             60.7%;  Score 412.5;  DB 11;  Length 233;
Best Local Similarity   69.2%;  Pred. No. 1.1e-37;
Matches   81;  Conservative  10;  Mismatches  25;  Indels  1;  Gaps  1;

Qy  11 LLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHY 70
         || |:|||||||||||||||||||||  |||| :| |: |:|||||||:  :||||||:|
Db  10 LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSGQIANYLNWYQQKPDGTVKLLIYY 69
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Qy  71 TSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         ||: |:|||||||||||||   ||||| |||||||||||  : |: |||||||||||
Db  70 TSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIK 126

RESULT 4
Q91WF8
ID   Q91WF8        PRELIMINARY;       PRT;   234 AA.
AC   Q91WF8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015292; AAH15292.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25929 MW;  B0D0B0E6EB7812D2 CRC64;

Query Match             60.4%;  Score 410.5;  DB 11;  Length 234;
Best Local Similarity   64.6%;  Pred. No. 1.8e-37;
Matches   82;  Conservative  14;  Mismatches  30;  Indels  1;  Gaps  1;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         |||||| |||| |:||||||||||||||||||||||:: |||| :| ||:|:|:  :|::
Db   1 MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP 60

Qy  61 GKRPLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGG 119
         :|||:||:|: :|:||||||||||||| :||| |||||:||||||:||:| :   :|||
Db  61 DGTVKLLIYYTSRLYLGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGS 120

Qy 120 GTKLEIK 126
         |||:||
Db 121 GTKLEVK 127

RESULT 5
Q9UL77
ID   Q9UL77        PRELIMINARY;       PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
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Left column:

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DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;   11738 MW;   C06681716C4D16F3 CRC64;

Query Match            57.3%;   Score 389.5;   DB 4;   Length 108;
Best Local Similarity  68.2%;   Pred. No. 1.6e-35;
Matches   73;   Conservative  13;   Mismatches  20;   Indels   1;   Gaps   1;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
             |||||||||| :|||| :||| : |:|:|| || ||| |:|| ||| |:|| |:||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK  126
             ||||||| | |:: :|||:|||| |||||  |   ||| |||:|||
Db   61  RFSGSGSGTDFTLTISSLQPEDFATYYCCQSYSTSWTFGEGTKVEIK  107


RESULT 6
Q96SA9
ID   Q96SA9;
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1
FT   NON_TER     107     107
SQ   SEQUENCE   107 AA;   11520 MW;   4BB43E9C5B577F16 CRC64;

Query Match            56.9%;   Score 387;   DB 4;   Length 107;
Best Local Similarity  67.9%;   Pred. No. 2.9e-35;
Matches   72;   Conservative  15;   Mismatches  19;   Indels   0;   Gaps   0;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
             |||||||||| :|||| : :||| : |:|:|| || ||| |:|| |||:|:||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK  126
             |||||||| : :|:: :|||:|:||| ||| : |||| ||||||
Db   61  RFSGSGSGTDFTLTISSLQPEDFATYYCCQSYSTLTFGGGTKVEIK  106


RESULT 7
Q9R1A5
ID   Q9R1A5;
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Kappa light chain of Mab7 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
```

Right column:

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RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1
FT   NON_TER     214     214
SQ   SEQUENCE   214 AA;   23922 MW;   52BA205FDE995E2A CRC64;

Query Match            56.0%;   Score 380.5;   DB 11;   Length 214;
Best Local Similarity  67.3%;   Pred. No. 3.5e-34;
Matches   72;   Conservative  14;   Mismatches  20;   Indels  20;   Gaps   1;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
             ||||:||||| :||| :||| | :| :|| || ||| |:|| |:||
Db    1  DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
             |||||||| |:: :|| :| || ||||| |:||  |||||||||||
Db   61  RFSGSGSGQDYSLRISSLEYEDMGIYYCLQYDEFPTFGGGTKLEIK  107


RESULT 8
Q9UL70
ID   Q9UL70;
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827713; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;   11633 MW;   B7BEDC3E41FCCA37 CRC64;

Query Match            55.7%;   Score 378.5;   DB 4;   Length 108;
Best Local Similarity  67.3%;   Pred. No. 2.6e-34;
Matches   72;   Conservative  16;   Mismatches  18;   Indels   1;   Gaps   1;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
             |||||||||| :|||| :|| || : | :|| || ||: ||| |:|| |:||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
             ||||||| :|:: :|||:||:|:|  ||| :||  |||||||
Db   61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFP...
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Db    61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107

RESULT 9
Q8VCP0
ID   Q8VCP0        PRELIMINARY;      PRT;    234 AA.
AC   Q8VCP0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019474; AAH19474.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003599; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   234 AA;   25702 MW;   1O251C58AC2FA9F CRC64;

Query Match            55.1%;  Score 374.5;  DB 11;  Pred. No. 1.8e-33;
Best Local Similarity  58.2%;  Pred. No. 1.8e-33;
Matches  71;  Conservative  20;  Mismatches  30;  Indels  1;  Gaps  1;

Qy    6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
          | |||| |:|||||||||||||||||| |||||:: |:||||| |:||::
Db    6 QVLGLLLCLTGARCDIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQ 65

Qy   66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE 124
          ||: | ||||||||||||||||||||:| |:|| |||||:|||||| |: ||||||||
Db   66 LLVYNAKTLADGVPSRFSGSGSRSGTQFSLKINSLQPEDFGSYYCQHHSGIPFTFGSGTKLE 125

Qy  125 IK 126
          ||
Db  126 IK 127

RESULT 10
Q9JL84
ID   Q9JL84        PRELIMINARY;      PRT;    107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206022; AAF69320.1; -.
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DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
FT   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
SQ   NON_TER    107    107
SQ   SEQUENCE   107 AA;   11648 MW;   ACF9B1253ACA1E5D CRC64;

Query Match            54.8%;  Score 372.5;  DB 11;  Length 107;
Best Local Similarity  68.2%;  Pred. No. 1.2e-33;
Matches  73;  Conservative   7;  Mismatches  26;  Indels  1;  Gaps  1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          ||||| |||||||| :|:|||||: |:|:| |:|:||:|||||: ||:|:|
Db    1 DIQMTQSTSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYTSSLXSGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
          |||||||| ||| ||||||||||||||| |: ||||||||||
Db   61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107

RESULT 11
Q925S9
ID   Q925S9        PRELIMINARY;      PRT;    127 AA.
AC   Q925S9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Immunoglobulin light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=99306687; PubMed=10380019;
RA   Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA   Foon K.A., Chatterjee S.K.;
RT   "Construction and characterization of a chimeric fusion protein
RT   consisting of an anti-idiotype antibody mimicking a breast cancer-
RT   associated antigen and the cytokine GM-CSF.";
RL   Hybridoma 18:193-202(1999).
DR   EMBL; AF124721; AAK55120.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER    127    127
SQ   SEQUENCE   127 AA;   13794 MW;   13F61BEBB981FA5 CRC64;

Query Match            54.0%;  Score 367.5;  DB 11;  Length 127;
Best Local Similarity  59.1%;  Pred. No. 5.2e-33;
Matches  75;  Conservative  14;  Mismatches  37;  Indels  1;  Gaps  1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          ||  |:||||:|| ||| ||||||||||||||||||||||||||||||||||||||
Db    1 MRAPAQILGFLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
          |||| |||||||||||||||:||:|| |||||||||||||:||| ::|| :|||
Db   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120

Qy  120 GTKLEIK 126
          |||||||
Db  121 GTKLEIK 127

RESULT 12
Q9UL81
ID   Q9UL81        PRELIMINARY;      PRT;    107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;   11501 MW;  070549FDE0754748 CRC64;

Query Match      53.2%;  Score 362;  DB 4;  Length 107;
Best Local Similarity   64.2%;  Pred. No. 1.7e-32;
Matches  68;  Conservative  15;  Mismatches  23;  Indels   0;  Gaps   0;

Qy       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            |||||||||||||||:| :||||| :: |:| |||| :||| | ||:  |:|:| |:||
Db        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy       81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
            |||||||| :: || || |||||| | ||||:| : ||||||||:|
Db       61 RFSGSGSGTDFTLTISCLQAEDFATYYCQQSYSALFGPGTKVDIR 106
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```
RESULT 13
ID   Q920E6        PRELIMINARY;       PRT;     109 AA.
AC   Q920E6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Pterin-mimicking anti-idiotope kappa chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307938; AAL09422.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;   11943 MW;  DAD3F98E05DD1501 CRC64;

Query Match      52.1%;  Score 354.5;  DB 11;  Length 109;
Best Local Similarity   61.7%;  Pred. No. 1.2e-31;
Matches  66;  Conservative  15;  Mismatches  25;  Indels   1;  Gaps   1;

Qy       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            ||||||||||||||:| |||||| :: |:| |||| || | :|||| |:|:| |:||
Db        1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 60

Qy       81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
```

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DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11787 MW;  DB5845F19724FB4E CRC64;

Query Match      51.0%;  Score 346.5;  DB 4;   Length 108;
Best Local Similarity   64.5%;  Pred. No. 9.2e-31;
Matches  69;  Conservative  12;  Mismatches  25;  Indels   1;  Gaps   1;

Qy       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            | |||||| |||||||| :|||:|| :|:|:| || |:||| | ||:| |:||
Db        1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy       81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
            |||||||| :: || || |||||| | ||||:| | ||||||||:||
Db       61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYSFPPTFGQGTKVEIK 107
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RESULT 15
ID   Q9QYF0        PRELIMINARY;       PRT;     298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CN 8 scFv.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RX   MEDLINE=20183931; PubMed=10706631;
RA   Shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a vascular cell wall-specific monoclonal antibody
RT   recognizing a cell polarity by using a phage display subtraction
RT   method.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
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RESULT 14
ID   Q9UL79        PRELIMINARY;       PRT;     108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
```

```
Db       61 RFSGSGSGTQYSLKINSLQPEDFGSYCQHFWSTPWTFGGGTKLEIK 107
```

```
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;   31867 MW;   E0F96B8A17004317 CRC64;

Query Match         50.2%;  Score 341.5;  DB 11;  Length 298;
Best Local Similarity   57.7%;  Pred. No. 1.1e-29;
Matches   64;  Conservative  18;  Mismatches  28;  Indels   1;  Gaps    1;

Qy    17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
            |  ||::||||:||||||:|  |||||: :|: |:||||  |  || |:||::|     |
Db   169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKGKSPQLLVYNAKTLAD 228

Qy    77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
           |:||||||||| |  |::|:||  :||| :  ::| |||||||||||||||
Db   229 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279

Search completed: January  6, 2003, 13:17:26
Job time : 25.6727 secs
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              GenCore version 5.1.3
      Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      January 6, 2003, 12:46:55 ; Search time 32.5253 Seconds
                                          (without alignments)
                                          573.557 Million cell updates/sec

Title:       US-09-155-739-4
Perfect score: 746
Sequence:    1 MKCSWVMFFLMAVVTGVNSE.........YCNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:        908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	746	100.0	140	16	AAR81327	Mouse VLA-4 antibo
2	746	100.0	140	18	AAW22410	Alpha-4 integrin m
3	645	86.5	123	16	AAR81330	Mouse anti-VLA-4 a
4	633	84.9	136	17	AAW04379	Chimaeric human/mu
5	629	84.3	140	12	AAR11384	Variable gamma hea
6	625	83.8	136	16	AAR76664	Murine ONS-21 anti
7	595	79.8	136	14	AAR41679	V heavy chain of r
8	593.5	79.6	137	18	AAR21845	Heavy chain variab
9	591	79.2	138	19	AAW63828	Human Mab #117-10C
10	584	78.3	142	16	AAR81333	Human VLA-4 reshap
11	584	78.3	142	18	AAW22428	Humanised alpha-4
12	576.5	77.3	135	21	AAB07967	Amino acid sequenc
13	570.5	76.5	137	17	AAR95948	HNK-20 variable he
14	544	72.9	123	16	AAR81323	Humanized VLA-4 an
15	539.5	72.3	135	21	AAB07969	A heavy chain vari
16	537	72.0	123	18	AAW22413	Humanised alpha-4
17	535.5	71.8	437	19	AAW37738	Nucleotide sequenc
18	524.5	70.3	122	21	AAY53590	Heavy chain from a
19	521.5	69.9	120	14	AAR30767	Heavy chain variab
20	521.5	69.9	120	19	AAW44121	Heavy chain variab
21	521.5	69.9	120	23	AAU79031	Mouse antibody NR-
22	518.5	69.5	113	15	AAR60527	Heavy chain variab
23	517	69.3	143	15	AAR59942	Anti-VLA4 rAb huma
24	516.5	69.2	120	16	AAR79889	Anti-EGFR antibody
25	516	69.2	121	20	AAW96741	Heavy chain variab
26	513	68.8	121	20	AAW96744	Heavy chain variab
27	513	68.8	138	22	AAG66455	VEGF ScFv protein
28	511	68.5	120	14	AAR39817	HP1/2 Vh. Homo sa
29	511	68.5	120	15	AAR58749	Anti-VLA4 Ab HP1/2
30	511	68.5	120	20	AAY23984	Antibody HP1/2 hea
31	511	68.5	120	20	AAY01033	Anti VLA-4 antibod
32	511	68.5	120	22	AAB73462	Murine anti-VLA-4
33	509.5	68.3	126	12	AAR15439	Heavy chain variab
34	508	68.1	120	14	AAR39566	Sequence of the va
35	507.5	68.0	133	23	ABB75617	Anti-RANK ligand m
36	505.5	67.8	138	21	AAY56873	MAb CT-M-01 heavy
37	505.5	67.8	139	18	AAW29750	Anti-HMFG MAb CTMO
38	504	67.6	254	20	AAY30117	Murine anti-botuli
39	504	67.6	254	20	AAY30119	Murine anti-botuli
40	504	67.6	254	20	AAY30121	Murine anti-botuli
41	504	67.6	254	20	AAY30123	Murine anti-botuli
42	503	67.4	136	22	AAB82701	VEGF antagonist an
43	502	67.3	136	16	AAR76681	Human/murine chime
44	502	67.3	136	17	AAW04396	Chimaeric human/mu
45	501.5	67.2	116	12	AAR15437	Heavy chain variab

ALIGNMENTS

```
RESULT 1
AAR81327
ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /note= "framework region 4"
XX
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PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
     leukocyte adhesion to endothelial cells, partic. for treating
     inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence 140 AA;

Query Match   100.0%; Score 746; DB 16; Length 140;
Best Local Similarity   100.0%; Pred. No. 9.6e-60;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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Db   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy 121 YGNYGVYAMDYWGQGTSVTv 140
         ||||||||||||||||||||
Db 121 YGNYGVYAMDYWGQGTSVTv 140

RESULT 2
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997   (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= Leader
FT   Region   20..49
FT   /label= FR1
FT   /note= "framework region 1"
FT   Region   50..54
FT   /label= CDR1
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /label= FR2
FT   /note= "framework region 2"
FT   Region   69..85
FT   /label= CDR2
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "framework region 3"
FT   Region   118..131
FT   /label= CDR3
FT   /note= "complementarity determining region 3"
FT   Region   132..140
FT   /label= FR4
FT   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
     asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence 140 AA;

Query Match   100.0%; Score 746; DB 18; Length 140;
Best Local Similarity   100.0%; Pred. No. 9.6e-60;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||||||||
Db  121 YGNYGVYAMDYWGQGTSVTV 140
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RESULT 3
AAR81330
ID   AAR81330 standard; Protein; 123 AA.
XX
AC   AAR81330;
XX
DT   02-APR-1996 (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /label= FR1
FT   /note= "mouse heavy chain variable framework
FT   region 1"
FT   Region   31..35
FT   /label= CDR1
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 1"
FT   Region   36..49
FT   /label= FR2
FT   /note= "mouse heavy chain variable framework
FT   region 2"
FT   Region   50..66
FT   /label= CDR2
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 2"
FT   Region   67..98
FT   /label= FR3
FT   /note= "mouse heavy chain variable framework
FT   region 3"
FT   Region   99..112
FT   /label= CDR3
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 3"
FT   Region   113..123
FT   /label= FR4
FT   /note= "mouse heavy light chain variable framework
FT   region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 68; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;

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Query Match             86.5%;  Score 645;  DB 16;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 1.1e-50;
Matches  121;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy  140 V 140
          |
Db  121 V 121
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RESULT 4
AAW04379
ID   AAW04379 standard; Protein; 136 AA.
XX
AC   AAW04379;
XX
DT   04-DEC-1996 (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 variable heavy region.
XX
KW   Heavy; variable region; murine; human; myeloblastoma; chimaera;
KW   monoclonal antibody; chimera; single stranded Fv region;
KW   low human antigenicity; diagnosis; treatment; cerebral tumour;
KW   reshaped.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= sig_peptide
FT   Peptide   20..136
FT   /label= mat_peptide
FT   Region   50..54
FT   /label= CDR_1
FT   Region   69..85
FT   /label= CDR_2
FT   Region   118..125
FT   /label= CDR_3
XX
PN   JP08169900-A.

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XX
PD   02-JUL-1996.
XX
PD   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38600.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 2; Page 22; 45pp; Japanese.
XX
CC   The present sequence is the variable heavy region of the
CC   chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb
CC   was prepd. by combining light and heavy variable region DNA,
CC   from a murine anti-human myeloblastoma cell MAb, with human light
CC   and heavy constant region sequences, respectively to produce
CC   chimaeric human/murine light and heavy chain DNA mols.. A
CC   recombinant vector for the expression of the heavy and light chain
CC   DNA mols. was prepd., and used to transform a host cell. The host
CC   cell was then cultured, and the expression prods. of the heavy and
CC   light chain DNA mols. sepd. and connected with a peptide linker to
CC   produce a single stranded Fv region. The reshaped Fv region has
CC   low human antigenicity, and is therefore expected to be useful as
CC   an agent for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

Query Match             84.9%;  Score 633;  DB 17;  Length 136;
Best Local Similarity   89.3%;  Pred. No. 1.5e-49;
Matches   125;  Conservative    2;  Mismatches    2;  Indels    6;  Gaps   2;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWAKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     61 EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAYYYCA-SAY 119

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          | |         ||||||||
Db    120 YVN-----QDYWGQGTSVTV 134

RESULT 5
AAR11384
ID   AAR11384 standard; Protein; 140 AA.
XX
AC   AAR11384;
XX
DT   08-MAY-1991 (first entry)
XX
DE   Variable gamma heavy chain of T84.66 monoclonal antibody.
XX
KW   MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
KW   human adenocarcinoma; mouse-human chimaeric antibody.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         20..38
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Peptide         39..49
```

```
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Peptide         55..59
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Region          50..54
FT                   /label= complementarity determining region
FT   Region          69..85
FT                   /label= complementarity determining region
FT   Region          118..130
FT                   /label= complementarity determining region
XX
PN   WO9101990-A.
XX
PD   21-FEB-1991.
XX
PF   19-JUL-1990;   90WO-US04049.
XX
PR   26-JUL-1989;   89US-0385102.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Shively JE,  Riggs AD,  Neumaier M;
XX
DR   WPI; 1991-073486/10.
DR   N-PSDB; AAQ11098.
XX
PT   Novel anti-CEA antibody - comparable to ATCC Accession No. BH
PT   8747, produced by recombinant DNA, used in diagnosis of tumours
XX
PS   Claim 4; Page 18; 24pp; English.
XX
CC   The heavy chain variable region of murine MAb 84.66 was cloned and
CC   sequenced. It was used to produce mouse V-human C antibodies with high
CC   affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to
CC   diagnose human colon adenocarcinomas.
CC   See also AAQ10834-Q10848.
XX
SQ   Sequence   140 AA;

Query Match             84.3%;  Score 629;  DB 12;  Length 140;
Best Local Similarity   87.9%;  Pred. No. 3.5e-49;
Matches   123;  Conservative    6;  Mismatches    9;  Indels    2;  Gaps   1;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |||||:|||||||||||||||||||||||||:|||||||||||||||||||:||||
Db      1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVEPGASVKLSCTASGFNIKDTYMHWVKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||||||||||| :|||||||||||||||||||||||||||||||||:|||||||
Db     61 EQGLEWIGRIDPANGNSKYVPKFQGKATITADTSSNTAYLQLTSLTSEDTAVYYCAPFGY 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          ||| ||||||||||||
Db    121 Y--VSDYAMAYWGQGTSVTV 138

RESULT 6
AAR76664
ID   AAR76664 standard; Protein; 136 AA.
XX
AC   AAR76664;
XX
DT   16-JAN-1996 (first entry)
XX
DE   Murine ONS-21 antibody variable heavy chain.
XX
KW   Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
```

FT   Peptide   1..19
FT   /label= sig_peptide
FT   Peptide   20..136
FT   /label= mat_peptide
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94485.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 14; Page 59; 120pp; Japanese.
XX
CC   AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the
CC   murine antibody ONS-21 variable heavy chain. The plasmid was
CC   used in the construction of an expression vector, contg. cDNA
CC   encoding a human/murine chimeric antibody, reactive with
CC   human medulloblastoma (a brain tumour) cells. The chimeric
CC   antibody can be used in the diagnosis and treatment of this
CC   disease.
XX
SQ   Sequence 136 AA;

Query Match   83.8%; Score 625; DB 16; Length 136;
Best Local Similarity   88.6%; Pred. No. 7.7e-49;
Matches 124; Conservative   2; Mismatches   8; Indels   6; Gaps   2;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              ||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGARAELVKPGASVKLSCTASGFNIKDTYIHWAKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              ||||||||||:| ||||||||||||||||||||||||||||||||||::||
Db   61 EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA-SAY 119

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
               || |||||||||
Db   120 YVN-----QDYWGQGTSVTV 134

RESULT 7
AAR41679
ID   AAR41679 standard; Protein; 136 AA.
XX
AC   AAR41679;
XX
DT   24-MAR-1994 (first entry)
XX
DE   V heavy chain of recombinant anti-feline calcivirus antibody.
XX
KW   Antibody; feline calcivirus; FCV; neutralise; heavy chain; virus;
KW   infection; diagnosis; treatment; prophylaxis.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Domain   47..54
FT   /label= Complementary Determining Region 1.
FT   Domain   69..86
FT   /label= Complementary Determining Region 2.

FT   Domain   118..125
FT   /label= Complementary Determining Region 3.
XX
PN   EP561194-A.
XX
PD   22-SEP-1993.
XX
PF   26-FEB-1993;   93EP-0103066.
XX
PR   28-FEB-1992;   92JP-0079189.
XX
PA   (KAGA) CHEMO SERO THERAPEUTIC RES INST.
XX
PI   Kimachi K, Maeda H, Mikami T, Nishiyama K, Tohya Y;
PI   Tokiyoshi S;
XX
DR   WPI; 1993-296521/38.
DR   N-PSDB; AAQ48001.
XX
PT   Anti-feline calcivirus recombinant antibody - used to treat,
PT   prevent and diagnosis infection and is safe but effective in cats
XX
PS   Claim 1-2; Figure 3; 36pp; English.
XX
CC   The gene fragment encoding the V heavy chain region is used to
CC   produce a genetically engineered antibody capable of reacting
CC   specifically with feline calcivirus (FCV). The antibody can be used
CC   to treat, prevent and diagnose FCV infection. It has a broad virus-
CC   neutralising spectrum and can be used to neutralise viruses which
CC   have acquired immunity to other neutralising antibodies.
XX
SQ   Sequence 136 AA;

Query Match   79.8%; Score 595; DB 14; Length 136;
Best Local Similarity   82.9%; Pred. No. 3.9e-46;
Matches 116; Conservative   8; Mismatches 10; Indels   6; Gaps   1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              ||||||:|||||||||||||||||||||||||||||:|||||||||||||||::| ||||
Db   1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVRLSCTASGFNIKDTYMHVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              |||||||||||||| ||||||::||||||||||||::|||||||||:||||::||:|
Db   61 EQGLEWIGRIDPANGNTKYDPRFQGKATITADTSFNTAYLQVNSLTSEDTAVYYCASGGN 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
               : |||||| |||
Db   121 AW------LAYWGQGTLVTV 134

RESULT 8
AAW21845
ID   AAW21845 standard; Protein; 137 AA.
XX
AC   AAW21845;
XX
DT   19-DEC-1997 (first entry)
XX
DE   Heavy chain variable region of KM1486 antibody.
XX
KW   Complementarity determining region; CDR; heavy chain; treatment;
KW   variable region; murine; mouse; human; interleukin 5; IL-5;
KW   receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW   assay; diagnosis; allergic respiratory disease;
KW   chronic bronchitis.
XX
OS   Mus spp.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= sig_peptide
FT   Peptide   20..137
FT   /label= mat_peptide

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FT   Region            50..54
FT                     /label= complementarity_determining_region_1
FT   Region            69..85
FT                     /label= complementarity_determining_region_2
FT   Region            118..126
FT                     /label= complementarity_determining_region_3
XX
PN   WO9710354-A1.
XX
PD   20-MAR-1997.
XX
PF   11-SEP-1996;   96WO-JP02588.
XX
PR   11-SEP-1995;   95JP-0232384.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
PI   Nakamura K, Takatsu K;
XX
DR   WPI: 1997-202249/18.
DR   N-PSDB; AAT73612.
XX
PT   Antibody against alpha-chain of human interleukin 5 receptor -
PT   useful for diagnosis and treatment of respiratory allergic diseases,
PT   e.g. chronic bronchitis
XX
PS   Example 2; Pages 124-125; 238pp; Japanese.
XX
CC   The present sequence is the heavy chain variable region of the
CC   murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
CC   monoclonal antibody (MAb) KM1486. KM1486 is produced by the hybridoma
CC   FERM BP-5651, which was prepared by immunising Balb/c mice with
CC   hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC   myeloma P3-U1 cells and screening the resultant hybridomas. The MAb
CC   can be used to detect or assay for hIL-5R alpha and cells
CC   expressing it on their surface, especially to diagnose allergic
CC   respiratory diseases, e.g. chronic bronchitis. It can also be used
CC   to treat such diseases.
XX
SQ   Sequence 137 AA;

Query Match             79.6%;  Score 593.5;  DB 18;  Length 137;
Best Local Similarity   82.9%;  Pred. No. 5.4e-46;
Matches  116;  Conservative   6;  Mismatches  13;  Indels   5;  Gaps 1;

Qy          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              |||||:||||||||||||||||||||||||||||||||||||||||||:|||
Db          1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRP 60

Qy         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              ||||||:|||||| ||| |||||| || |||||||||||||||||||||||||:
Db         61 EQGLEWIGRIDPANGNTKSDPKFQAKATIADTSSNTAYLQLSSLTSEDTAVYYCT----  116

Qy        121 YGNYGVYAMDYWGQGTSVTV 140
                ||:| |||||::||
Db        117 -GGLRLRFFDYWGQGTTLTV 135

RESULT 9
AAW63828
ID   AAW63828 standard; Protein; 138 AA.
XX
AC   AAW63828;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Human Mab #117-10C heavy chain variable region protein fragment.
XX
KW   Interleukin-18; IL-18; human; treatment; autoimmune disease; Mab;
KW   immunosuppressant; inhibitor; receptor protein; detection; heavy chain;
KW   monoclonal antibody; Mab; variable region.
XX
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OS   Homo sapiens.
XX
FH   Key                 Location/Qualifiers
FT   Peptide             1..19
FT                       /label= signal
FT   Protein             20..138
FT                       /label= Mab 117-10C heavy chain variable region
XX
PN   EP850952-A1.
XX
PD   01-JUL-1998.
XX
PF   23-DEC-1997;   97EP-0310555.
XX
PR   28-JUL-1997;   97JP-0215490.
PR   26-DEC-1996;   96JP-0356426.
PR   21-FEB-1997;   97JP-0052526.
PR   06-JUN-1997;   97JP-0163490.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Kunikata T, Kurimoto M, Torigoe K, Ushio S;
XX
DR   WPI: 1998-335317/30.
DR   N-PSDB; AAV44000.
XX
PT   New interleukin-18 receptor protein used to inhibit interleukin-18,
PT   to treat autoimmune disease and as immunosuppressant - and new
PT   monoclonal antibody and hybridoma used to detect interleukin -18
PT   receptor protein
XX
PS   Example 3.3a; Page 22; 35pp; English.
XX
CC   This sequence represents the human monoclonal antibody (Mab) #117-10C
CC   heavy chain variable region which is used in a method involved in
CC   neutralising IL-18 or to treat autoimmune diseases or as an
CC   immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
CC   Such antibodies can also be used to detect the IL-18 receptor protein
CC   (labelled with an enzyme or a radioactive or fluorescent substance). The
CC   protein is used to treat e.g. graft rejection, pernicious anaemia,
CC   atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,
CC   discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating
CC   diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic
CC   ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
CC   syndrome, autoimmune haepatitis, autoimmune haemolytic anaemia, myasthenia
CC   gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic
CC   cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple
CC   sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease,
CC   leukopaenia, Behcet's disease, climacterium praecox, rheumatoid
CC   arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
CC   asthma, atopic dermatitis, allergic nastitis, pollinosis,
CC   apitoxin-allergy and septic shock resulting from production or
CC   administration of excessive gamma interferon (IFN-gamma).
XX
SQ   Sequence 138 AA;

Query Match             79.2%;  Score 591;  DB 19;  Length 138;
Best Local Similarity   83.0%;  Pred. No. 9.1e-46;
Matches  117;  Conservative   4;  Mismatches  14;  Indels   6;  Gaps 2;

Qy          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              ||||| |||||||||||||||||||||||||||||||||||||||||:|||
Db          1 MKCSWVLFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTTSGFNIKDIYIYWVKQRP 60

Qy         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              |||||||:|||||||||| ||||||||||||||||||||||||||||||:||| |
Db         61 EQGLEWVGRIDPANGDTKYGPNFQDKATITADTSSNTAYLQLRSLTSEDTAVYYCARRGN 120

Qy        121 YG-NYGVYAMDYWGQGTSVTV 140
                ||  :|  |||||:|| |||
Db        121 YGAGFG----YWGQGTLVTV 136
```

RESULT 10
AAR81333
ID   AAR81333 standard; Protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanised antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT
FT   Peptide   1..19
FT   /note= "signal peptide"
FT   Region   20..49
FT   /note= "framework region 1"
FT   Region   50..54
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /note= "framework region 2"
FT   Region   69..85
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /note= "framework region 3"
FT   Region   118..131
FT   /note= "complementarity determining region 3"
FT   Region   132..142
FT   /note= "framework region 4"
XX
PN   WO9519790-Al.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions. In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX

SQ   Sequence   142 AA;

Query Match   78.3%; Score 584; DB 16; Length 142;
Best Local Similarity   77.1%; Pred. NO. 4e-45;
Matches 108; Conservative   15; Mismatches   17; Indels   0; Gaps   0:

Qy   1 MKCSWVMFFLMAVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           : | :|| | : | :|:||| ||||: |||||||:|| |||||||||:|:|
Db   1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTIHWVRQAP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           | ||:||||||||||||||||||||: |||||||: ||||:::||:|||:|||| |||||||
Db   61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||| |||
Db   121 YGNYGVYAMDYWGQGTLVTV 140

RESULT 11
AAW22428
ID   AAW22428 standard; Protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= Leader
FT   Protein   20..142
FT   /label= Mat_protein
FT   /note= "VH version Ha (Claim 25)"
FT   Region   20..49
FT   /label= FR1
FT   /note= "21/28'CL framework region 1"
FT   Region   50..55
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   55..67
FT   /label= FR2
FT   /note= "21/28'CL framework region 2"
FT   Region   68..85
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "21/28'CL framework region 3"
FT   Region   118..131
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
FT   Region   132..142
FT   /label= FR4
FT   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-Al.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.

XX
FT   Protein   /note= "signal peptide"
FT   20..135
FT   Region   /note= "mature protein"
FT   50..54
FT   Region   /note= "complementarity determining region 1"
FT   69..85
FT   Region   /note= "complementarity determining region 1"
FT   118..124
FT   Region   /note= "complementarity determining region 1"
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999;   99US-0249011.
PR   24-JUN-1999;   99US-0339596.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI   Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR   WPI; 2000-524532/47.
DR   N-PSDB; AAA59696.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC pTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases -
XX
PS   Example 8; Fig 6A; 162pp; English.
XX
CC   The present sequence represents the heavy chain variable region of the
CC   murine antibody 1F1. The antibody has a binding specificity to B7
CC   molecules. The antibody is used to construct humanized immunoglobulins,
CC   which comprise an antigen binding region of non-human origin and a
CC   portion of a human immunoglobulin. The humanized immunoglobulins are
CC   useful for treating autoimmune diseases, infectious diseases,
CC   inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence 135 AA;

Query Match   77.3%; Score 576.5; DB 21; Length 135;
Best Local Similarity   80.7%; Pred. No. 1.8e-44;
Matches 113; Conservative   6; Mismatches   14; Indels   7; Gaps   1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||||||||||||||||||||||| |||||||:||||| ||||||||||:|:||||||
Db   1 MKCSWVIFFLMAVVTGVNSEVHLQQSGAELVRPGALVKLSCKPSGFNIKDYYMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db   61 EQGLEWIGWIDPENGNTLYDPKFQGKASITADTSSNTAYLQLSSLTSEDTAVYYCAREGL 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
         || |||| |||||||| |||
Db 121 F------FAYWGQGTPVTV 133

RESULT 13
AAR95948
ID   AAR95948 standard; Protein; 137 AA.
XX
AC   AAR95948;

RESULT 12
AAB07967
ID   AAB07967 standard; Protein; 135 AA.
XX
AC   AAB07967;
XX
DT   14-NOV-2000 (first entry)
XX
DE   Amino acid sequence of heavy chain variable region of 1F1 antibody.
XX
KW   Antibody 1F1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;
KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19

XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413). It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence 142 AA;

Query Match   78.3%; Score 584; DB 18; Length 142;
Best Local Similarity   77.1%; Pred. No. 4e-45;
Matches 108; Conservative   15; Mismatches   17; Indels   0; Gaps   0;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         | :| : |:|| | : :|:|| | ||| ||||||||||||||||||||||:|:|
Db   1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         | |||||||||||||||||||||||||:|||||:|:||| ||||||||||||||||||
Db   61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
         |||||||||||||||| |||
Db 121 YGNYGVYAMDYWGQGTLVTV 140

RESULT 14
AAR81323

XX
DT 10-FEB-1997 (first entry)
XX
DE HNK-20 variable heavy chain.
XX
KW Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse;
KW F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
KW chimeric antibody; isotype-switched antibody; therapy; infection; human;
KW pneumonia; bronchiolitis; animal.
XX
OS Mus musculus.
XX
PN WO9616974-A1.
XX
PD 06-JUN-1996.
XX
PF 01-DEC-1995;   95WO-US15716.
XX
PR 01-DEC-1994;   94US-0348548.
XX
PA (ORAV-) ORAVAX INC.
XX
PI Berdoz J, Kraehenbuhl J;
XX
DR WPI; 1996-286826/29.
DR N-PSDB; AAT30458.
XX
PT DNA encoding variable region of antibody HNK-20 - for treating
PT respiratory syncytial virus infection
XX
PS Claim 15; Fig 5d; 75pp; English.
XX
CC AAR95946-R95948 represent sequences for variable regions of an antibody
CC produced by the hybridoma cell line HNK-20. This sequence represents
CC the sequence for the antibody HNK-20 variable heavy chain. HNK-20 is a
CC murine hybridoma cell line, that produces IgA specific for the F
CC glycoprotein of respiratory syncytial virus (RSV). The DNA encoding
CC these sequences were isolated using primers specific for the 5'
CC untranslated region of the variable region, and for the intron
CC downstream of the rearranged J region (see AAT30459-T30545 for primer
CC sequences). The DNA encoding these sequences can be inserted into vectors
CC containing heterologous (such as human) constant region genes, for the
CC production of chimeric and isotype-switched antibodies. The antibodies
CC are useful in the treatment and diagnosis of infection by RSV, such as
CC pneumonia and bronchiolitis, in humans and animals. By using genomic DNA
CC as a template, variable region genes can be isolated without producing
CC fragments that have to be adapted for recombinant antibody expression.
CC Also, by using the genomic DNA, no knowledge of the DNA sequence
CC encoding the target variable region is required. Chimeric antibodies
CC produced from these proteins, that contain the constant region of the
CC host being treated, are less likely to cause adverse immune reactions.
XX
SQ Sequence 137 AA;

Query Match   76.5%; Score 570.5; DB 17; Length 137;
Best Local Similarity   81.4%; Pred. No. 6.4e-44;
Matches 114; Conservative   6; Mismatches 15; Indels   5; Gaps   2;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              |||||||| ||||||||||||||||||||||||||||||||||||: :|| ||||
Db   1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYMYWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              |||||||| || || |||||||||||||||||||||||||||||||:|| |
Db   61 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSNTAYLQLSSLASEDTAVYYCA---Y 117

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
              ||| ||||| |||
Db   118 YGT--SYWFPYWGQGTLVTV 135

RESULT 15
AAB07969

ID AAR81323 standard; Protein; 123 AA.
XX
AC AAR81323;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995;   95WO-US01219.
XX
PR 25-JAN-1994;   94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Claim 11; Page 69; 105pp; English.
XX
CC The sequence encodes the mouse antibody 21.6 heavy chain variable
CC region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC are linked to human constant regions in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC modified using PCR primers (See AAQ99895-98) and then subcloned into
CC mammalian cell expression vectors containing human kappa or gamma-1
CC constant regions. In the humanized light chain, amino acids L45,
CC L49, L58 and L69 in the human kappa LC VR framework are replaced
CC by the amino acid present in the equivalent position of the mouse
CC 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC transfected into COS cells. The humanized antibodies can be used
CC for inhibiting adhesion of a leukocyte to an endothelial cell and
CC for treating inflammatory diseases such as multiple sclerosis. They
CC can also be used in the treatment of stroke, cerebral traumas,
CC meningitis or encephalitis. The antibodies can also be used for
CC detecting VLA-4, for affinity purification or for generating
CC anti-idiotype antibodies.
XX
SQ Sequence 123 AA;

Query Match   72.9%; Score 544; DB 16; Length 123;
Best Local Similarity   82.6%; Pred. No. 1.4e-41;
Matches 100; Conservative 11; Mismatches 10; Indels   0; Gaps   0;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
              :|||||||||| |||||: ||||||||||||||||||:||| |||||||| ||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
              |||||||| |||||||||||||||||||||||||| |||||||||||||||||||||| |
Db   61 DPKFQGQRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy   140 V 140
              |
Db   121 V 121

```
ID   AAB07969 standard; Protein; 135 AA.
XX
AC   AAB07969;
XX
DT   14-NOV-2000  (first entry)
XX
DE   A heavy chain variable region of humanised 1F1 antibody.
XX
KW   Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;
KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Protein         20..135
FT                   /note= "mature protein"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          69..85
FT                   /note= "complementarity determining region 1"
FT   Region          118..124
FT                   /note= "complementarity determining region 1"
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999; 99US-0249011.
PR   24-JUN-1999; 99US-0339596.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Co MS,  Vasquez M,  Carreno B,  Celniker AC,  Collins M,   Goldman S;
PI   Gray GS,  Knight A,  O'hara D,  Rup B,  Veldman GM;
XX
DR   WPI; 2000-524532/47.
DR   N-PSDB; AAA59698.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases -
XX
PS   Example 10; Fig 7A; 162pp; English.
XX
CC   The present sequence represents the heavy chain variable region of the
CC   humanised murine antibody 1F1. The antibody has a binding specificity to
CC   B7 molecules. The antibody is used to construct humanized
CC   immunoglobulins, which comprise an antigen binding region of non-human
CC   origin and a portion of a human immunoglobulin. The humanized
CC   immunoglobulins are useful for treating autoimmune diseases, infectious
CC   diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence   135 AA;
```

```
Query Match              72.3%;  Score 539.5; DB 21; Length 135;
Best Local Similarity    75.0%;  Pred. No. 3.9e-41;
Matches  105; Conservative  11; Mismatches  17; Indels   7;  Gaps   1;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||:||:|||||||||||||||||: |||||||: ||||||| ||||||||:|| |:||:
Db     1 MKCSWVIFFLMAVVTGVNSEVQLVQSGAEVKKPGASVKVSCKPSGFNIKDYMHWVRQAP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         |:|||||:|| ||||: ||||||||||||||||:::||:::|||:|||||||:|||||||
Db    61 GQGLEWIGWIDPENGNTLYDPKFQGKATITADTSTSTAYMELSSLRSEDTAVYYCAREGL 120

Qy   121 YGNYGVYAMDYWGQTSVTV 140
         |||||| |||
Db   121 F------FAYWGQGTLVTV 133

Search completed: January  6, 2003, 13:15:16
Job time : 33.5253 secs
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OM protein - protein search, using sw model

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          GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: January 6, 2003, 13:13:21 ; Search time 11.596 Seconds
                                       (without alignments)
                                       355.228 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE..........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Issued_Patents.AA:*
    1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
    2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
    3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
    4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
    5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB	ID	Description
1	746	100.0	140	140	2	US-08-561-521-4	Sequence 4, Appli
2	746	100.0	140	140	5	PCT-US95-01219-4	Sequence 4, Appli
3	645	86.5	123	123	2	US-08-561-521-9	Sequence 9, Appli
4	645	86.5	123	123	5	PCT-US95-01219-9	Sequence 9, Appli
5	633	84.9	136	136	4	US-08-646-265A-29	Sequence 29, Appli
6	595	79.8	136	137	1	US-08-024-253-2	Sequence 2, Appli
7	593.5	79.6	137	142	2	US-08-836-561-31	Sequence 31, Appl
8	584	78.3	142	142	5	US-08-561-521-17	Sequence 17, Appl
9	584	78.3	142	142	5	PCT-US95-01219-17	Sequence 17, Appl
10	562	75.3	125	125	5	US-08-561-521-44	Sequence 44, Appl
11	562	75.3	125	125	5	PCT-US95-01219-44	Sequence 44, Appl
12	554	74.3	136	136	4	US-08-348-548-8	Sequence 8, Appli
13	554	74.3	136	136	5	PCT-US95-15716-8	Sequence 8, Appli
14	544	72.9	123	123	5	US-08-561-521-11	Sequence 11, Appl
15	544	72.9	123	123	5	PCT-US95-01219-11	Sequence 11, Appl
16	528.5	70.8	120	120	3	US-07-934-373C-6	Sequence 6, Appli
17	528.5	70.8	120	120	3	US-08-437-642B-6	Sequence 6, Appli
18	528.5	70.8	120	120	4	US-08-146-206C-6	Sequence 6, Appli
19	528.5	70.8	120	120	5	PCT-US93-07832-6	Sequence 6, Appli
20	521.5	69.9	120	120	4	US-08-871-488A-15	Sequence 15, Appl
21	516	69.2	121	121	2	US-08-822-830B-2	Sequence 2, Appli
22	513	68.8	121	121	2	US-08-822-830B-13	Sequence 13, Appl
23	511	68.5	120	120	2	US-08-950-660-2	Sequence 2, Appli
24	511	68.5	120	120	5	PCT-US93-00030-2	Sequence 2, Appli
25	511	68.5	120	120	5	PCT-US93-00924-2	Sequence 2, Appli
26	505.5	67.8	138	138	3	US-08-603-024-2	Sequence 2, Appli
27	505.5	67.8	139	139	1	US-08-253-877C-8	Sequence 8, Appli
28	505.5	67.8		139	2	US-08-452-164A-8	Sequence 8, Appli
29	504	67.6		254	2	US-08-792-824-4	Sequence 4, Appli
30	504	67.6		254	2	US-08-792-824-7	Sequence 7, Appli
31	504	67.6		254	2	US-08-792-824-10	Sequence 10, Appli
32	504	67.6		254	2	US-08-792-824-13	Sequence 13, Appl
33	502	67.3		136	4	US-08-646-265A-99	Sequence 99, Appl
34	500.5	67.1		118	2	US-08-232-081B-38	Sequence 38, Appl
35	498.5	66.8		113	1	US-08-207-169A-2	Sequence 2, Appli
36	494.5	66.3		118	3	US-08-767-128-22	Sequence 22, Appl
37	491.5	65.9		642	4	US-09-423-439-26	Sequence 26, Appl
38	491.5	65.9		666	4	US-09-423-439-51	Sequence 51, Appl
39	488.5	65.5		255	1	US-09-171-945-19	Sequence 19, Appl
40	483.5	64.8		139	2	US-08-182-067-10	Sequence 10, Appl
41	483.5	64.8		139	2	US-08-465-313-10	Sequence 10, Appl
42	482.5	64.7		139	2	US-08-039-198B-10	Sequence 10, Appl
43	475.5	63.7		137	1	US-08-477-877B-86	Sequence 86, Appl
44	475.5	63.7		137	2	US-08-472-281A-86	Sequence 86, Appl
45	475.5	63.7		137	2	US-08-477-989B-86	Sequence 86, Appl

ALIGNMENTS

```
RESULT 1
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;  APPLICANT:  Bendig, Mary M.
;  APPLICANT:  Leger, Olivier J.
;  APPLICANT:  Saldanha, Jose
;  APPLICANT:  Jones, S. Tarran
;  TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;  TITLE OF INVENTION:  Adhesion Molecule VLA-4
;  NUMBER OF SEQUENCES:  45
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend Khourie and Crew
;   STREET:  One Market Plaza, Steuart Tower, Suite 2000
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94105
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/561,521
;   FILING DATE:
;   CLASSIFICATION:  424
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/186,269A
;   FILING DATE:  25-JAN-1994
;  ATTORNEY/AGENT INFORMATION:
;   NAME:  Smith, William L.
;   REGISTRATION NUMBER:  30,223
;   REFERENCE/DOCKET NUMBER:  15270-14
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-543-9600
;   TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH:  140 amino acids
;    TYPE:  amino acid
;    TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-561-521-4

Query Match             100.0%;  Score 746;  DB 2;  Length 140;
Best Local Similarity   100.0%;  Pred. No. 1.8e-68;
  Matches  140;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
         ||||||||||||||||||||
Db   121 YGNYGVYAMDYWGQGTSVTV 140
```

RESULT 2
PCT-US95-01219-4
; Sequence 4, Application PCT/US9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-4

Query Match   100.0%; Score 746; DB 5; Length 140;
Best Local Similarity   100.0%; Pred. No. 1.8e-68;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
         ||||||||||||||||||||
Db   121 YGNYGVYAMDYWGQGTSVTV 140
```

RESULT 3
US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-9

Query Match   86.5%; Score 645; DB 2; Length 123;
Best Local Similarity   100.0%; Pred. No. 2.6e-58;
Matches 121; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy    80 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 120

Qy   140 V 140
         |
Db   121 V 121
```

RESULT 4
PCT-US95-01219-9
; Sequence 9, Application PCT/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose

```
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-9

Query Match             86.5%;  Score 645; DB 5; Length 123;
Best Local Similarity  100.0%;  Pred. No. 2.6e-58;
Matches  121; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy    80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVFCAREGYYGNYGVYAMDYWGQGTSVT 139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy   140 V 140
          |
Db   121 V 121

RESULT 5
US-08-646-265A-29
; Sequence 29, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
;   APPLICANT: OHTOMO, Toshihiko
;   APPLICANT: SATO, Koh
;   APPLICANT: TSUCHIYA, Masayuki
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
;   NUMBER OF SEQUENCES: 132
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,265A
;   FILING DATE: 09-SEP-1996
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP94/01763
;   FILING DATE: 19-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 5-291078
;   FILING DATE: 19-NOV-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/184
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 136 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-646-265A-29

Query Match             84.9%;  Score 633; DB 4; Length 136;
Best Local Similarity   89.3%;  Pred. No. 4.9e-57;
Matches  125; Conservative  2; Mismatches  7; Indels  6; Gaps  2;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWAKQRP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVFCAREGY 120
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||| |||
Db    61 EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYCA-SAY 119

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
          |.|      |||||||||
Db   120 YVN----QDYWGQGTSVTV 134

RESULT 6
US-08-024-253-2
; Sequence 2, Application US/08024253
; Patent No. 5785968
; GENERAL INFORMATION:
;   APPLICANT: KIMACHI, Kazuhiko
;   APPLICANT: MAEDA, Hiroaki
;   APPLICANT: NISHIYAMA, Kiyoto
;   APPLICANT: TOKIYOSHI, Sachio
;   APPLICANT: TOHYA, Yukinobu
;   APPLICANT: MIKAMI, Takeshi
;   TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
;   TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
;   STREET: 1233 20th Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20036-8218
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
```

```
         OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/08/024,253
         FILING DATE: 19930301
         CLASSIFICATION: 424
    PRIOR APPLICATION DATA:
         APPLICATION NUMBER: JP 79189/1992
         FILING DATE: 28-FEB-1992
    ATTORNEY/AGENT INFORMATION:
         NAME: CANTOR, Herbert I
         REGISTRATION NUMBER: 24,392
         REFERENCE/DOCKET NUMBER: P-500-23744
    TELECOMMUNICATION INFORMATION:
         TELEPHONE: (202) 887-0400
         TELEFAX: (202) 835-0605
         TELEX: 440706 WEGBR
INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
         LENGTH: 136 amino acids
         TYPE: amino acid
         TOPOLOGY: linear
         MOLECULE TYPE: protein
US-08-024-253-2

Query Match          79.8%;      Score 595;  DB 1;  Length 136;
Best Local Similarity 82.9%;     Pred. No. 3.5e-53;
Matches 116; Conservative 8;  Mismatches 10;  Indels 6;  Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        ||||| :||||||||||||||||||||||||||||||: ||||||||||||: ||||| ||||
Db   1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVRLSCTASGFNIKDTYMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATIADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        ||||||||||||||||| |||||| ||||| ::||||||||||: :|| ||||||||||||| 120
Db  61 EQGLEWIGRIDPANGNTKYDPRFQGKATITADTSFNTAYLQVNSLTSEDTAVYYCASGGN 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        |||||| ||| |||
Db 121 AW------LAYWGQGTLVTV 134

RESULT 7
US-08-836-561-31
; Sequence 31, Application US/08836561
Patent No. 6018032
GENERAL INFORMATION:
    APPLICANT: KOIKE, Masamichi
    APPLICANT: FURUYA, Akiko
    APPLICANT: NAKAMURA, Kazuyasu
    APPLICANT: IIDA, Akihiro
    APPLICANT: ANAZAWA, Hideharu
    APPLICANT: HANAI, No. 6018032uo
    APPLICANT: TAKATSU, Kiyoshi
    TITLE OF INVENTION: Antibody Against Human Interleukin-5
    TITLE OF INVENTION: Receptor Alpha Chain
    NUMBER OF SEQUENCES: 106
    CORRESPONDENCE ADDRESS:
         ADDRESSEE: Pennie & Edmonds LLP
         STREET: 1155 Avenue of the Americas
         CITY: New York
         STATE: NY
         COUNTRY: USA
         ZIP: 10036
    COMPUTER READABLE FORM:
         MEDIUM TYPE: Diskette
         COMPUTER: IBM Compatible
         OPERATING SYSTEM: DOS
         SOFTWARE: FastSEQ Version 2.0
    CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/08/836,561
         FILING DATE: 09-MAY-1997
         CLASSIFICATION: 424
```

```
    PRIOR APPLICATION DATA:
         APPLICATION NUMBER: JP 232384/95
         FILING DATE: 11-SEP-1995
    ATTORNEY/AGENT INFORMATION:
         NAME: Lawrence, III, Stanton T
         REGISTRATION NUMBER: 25,736
         REFERENCE/DOCKET NUMBER: 7005-115-999
    TELECOMMUNICATION INFORMATION:
         TELEPHONE: 212-790-9090
         TELEFAX: 212-869-9741
         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
    SEQUENCE CHARACTERISTICS:
         LENGTH: 137 amino acids
         TYPE: amino acid
         STRANDEDNESS: single
         TOPOLOGY: linear
         MOLECULE TYPE: peptide
US-08-836-561-31

Query Match          79.6%;      Score 593.5;  DB 3;  Length 137;
Best Local Similarity 82.9%;     Pred. No. 5.1e-53;
Matches 116; Conservative 6;  Mismatches 13;  Indels 5;  Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        ||||| :|||||||||||||||||||||||||||||: |||||||||||: ||||| ||||
Db   1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVNLSCTASGFNIKDTYMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATTADTSSNTAYIQLSSLTSEDTAVYFCAREGY 120
        |||||||||||||||: ||| |||| ||||:: ||||||||||||||||||||||||: |||
Db  61 EQGLEWIGRIDPANGNTKSDPKFQAKATIAADTSSNTAYIQLSSLTSEDTAVYYCT---- 116

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||  :::||
Db 117 -GGLRLRFFDYWGQGTTLTV 135

RESULT 8
US-08-561-521-17
; Sequence 17, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
    APPLICANT: Bendig, Mary M.
    APPLICANT: Leger, Olivier J.
    APPLICANT: Saldanha, Jose
    APPLICANT: Jones, S. Tarran
    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
    TITLE OF INVENTION: Adhesion Molecule VLA-4
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
         ADDRESSEE: Townsend and Townsend Khourie and Crew
         STREET: One Market Plaza, Steuart Tower, Suite 2000
         CITY: San Francisco
         STATE: California
         COUNTRY: USA
         ZIP: 94105
    COMPUTER READABLE FORM:
         MEDIUM TYPE: Floppy disk
         COMPUTER: IBM PC compatible
         OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/08/561,521
         FILING DATE:
         CLASSIFICATION: 424
    PRIOR APPLICATION DATA:
         APPLICATION NUMBER: US/08/186,269A
         FILING DATE: 25-JAN-1994
    ATTORNEY/AGENT INFORMATION:
         NAME: Smith, William L.
         REGISTRATION NUMBER: 30,223
         REFERENCE/DOCKET NUMBER: 15270-14
    TELECOMMUNICATION INFORMATION:
```

```
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 142 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-561-521-17

Query Match     78.3%;   Score 584;   DB 2;   Length 142;
Best Local Similarity 77.1%;   Pred. No. 4.9e-52;
Matches 108;   Conservative 15;   Mismatches 17;   Indels 0;   Gaps 0;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          :  : :| :|| : :|:|| |||| : ||||||:|||||:|| |||||||||||:|: |
Db    1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60
Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         |||||||||||||||||||||||||||:||::||| |||||:||||
Db   61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120
Qy  121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||| |||
Db  121 YGNYGVYAMDYWGQGTLVTV 140

RESULT 9
PCT-US95-01219-17
; Sequence 17, Application PCT/US9501219
; GENERAL INFORMATION:
;    APPLICANT: Bendig, Mary M.
;    APPLICANT: Leger, Olivier J.
;    APPLICANT: Saldanha, Jose
;    APPLICANT: Jones, S. Tarran
;    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION: Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES: 45
;    CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend Khourie and Crew
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;    COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US95/01219
;     FILING DATE: 25-JAN-1995
;     CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/186,269
;     FILING DATE: 25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William L.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-14
;    TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 142 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
PCT-US95-01219-17

Query Match     78.3%;   Score 584;   DB 5;   Length 142;
```

```
Best Local Similarity 77.1%;   Pred. No. 4.9e-52;
Matches 108;   Conservative 15;   Mismatches 17;   Indels 0;   Gaps 0;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          : |: :|| : :|:|| |||| : ||||||:|||||:|| |||||||||||:|: |
Db    1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60
Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         |||||||||||||||||||||||||||:||::||| |||||:||||
Db   61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120
Qy  121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||| |||
Db  121 YGNYGVYAMDYWGQGTLVTV 140

RESULT 10
US-08-561-521-44
; Sequence 44, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;    APPLICANT: Bendig, Mary M.
;    APPLICANT: Leger, Olivier J.
;    APPLICANT: Saldanha, Jose
;    APPLICANT: Jones, S. Tarran
;    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION: Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES: 45
;    CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend Khourie and Crew
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;    COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/561,521
;     FILING DATE:
;     CLASSIFICATION: 424
;    PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/186,269A
;     FILING DATE: 25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William L.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-14
;    TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 44:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 125 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-561-521-44

Query Match     75.3%;   Score 562;   DB 2;   Length 125;
Best Local Similarity 89.4%;   Pred. No. 7e-50;
Matches 110;   Conservative 2;   Mismatches 9;   Indels 2;   Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
        ||||||||||||||||||||||||||||||||||:||:|||||||||||||||||||:|||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60
Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY--GNYGVYAMDYWGQGTS 137
        ||||||||||||||||||||||||||||:||| ||  |  |||||||||||
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Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYDSXVGYYAMDYWGQGTX 120

Qy   138 VTV 140
         |||
Db   121 VTV 123

RESULT 11
PCT-US95-01219-44
; Sequence 44, Application PC/TUS9501219
GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 44:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 125 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-44

Query Match   75.3%;   Score 562; DB 5; Length 125;
Best Local Similarity   89.4%;   Pred. No. 7e-50;
Matches 110; Conservative   2; Mismatches   9; Indels   2; Gaps   1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY--GNYGVYAMDYWGQGTS 137
         |||||||||||||||||||||||||||| || ||||||| | ||||||||||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120

Qy   138 VTV 140
         |||
Db   121 VTV 123

RESULT 12
US-08-348-548-8
; Sequence 8, Application US/08348548

Patent No. 6258529
GENERAL INFORMATION:
;   APPLICANT: Berdoz, Jose
;   APPLICANT: Kraehenbuhl, Jean Pierre
;   TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
;   TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
;   NUMBER OF SEQUENCES: 108
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 225 Franklin Street, Suite 3100
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30B
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/348,548
;   FILING DATE: 01-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Clark, Paul T.
;   REGISTRATION NUMBER: 30,162
;   REFERENCE/DOCKET NUMBER: 06132/009001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 542-5070
;   TELEFAX: (617) 542-5070
;   TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 136 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-348-548-8

Query Match   74.3%;   Score 554; DB 4; Length 136;
Best Local Similarity   80.7%;   Pred. No. 5.1e-49;
Matches 113; Conservative   6; Mismatches 15; Indels   6; Gaps   3;

Qy   1 MKCSWVFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         |||||||||||| |||||||||||||||||| :||||||||||||||:|: ||||
Db   1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 59

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||| ||| |||||||||||||||:|||||||||||||||||||||||||:|| ::|
Db   60 EQGLEWIGWIDPENGNTVYDPKFQGKASTTADTSSNTAYLQLSSLASEDTAVYYCA---Y 116

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
         |||:|||| ||| ||||||
Db   117 YGT--SYWFPYWGQGTLVTV 134

RESULT 13
PCT-US95-15716-8
; Sequence 8, Application PC/TUS9515716
GENERAL INFORMATION:
;   APPLICANT: Berdoz, Jose
;   APPLICANT: Kraehenbuhl, Jean Pierre
;   TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
;   TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
;   NUMBER OF SEQUENCES: 108
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 225 Franklin Street, Suite 3100
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15716-8

Query Match        74.3%;  Score 554; DB 5;  Length 136;
Best Local Similarity 80.7%; Pred. No. 5.1e-49;
Matches 113; Conservative 6; Mismatches 15; Indels 6; Gaps 3;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         |||||||:||||| |||||||||||||||||| |:: ||||||| |::||||||||
Db   1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYMYWVKQRP 59

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||| | ||||||||:||||||||||||||||||||||| ||||||||:|
Db  60 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 116

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
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Db 117 YGT--SYWFPYWGQGTLVTV 134

RESULT 14
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:


APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-11

Query Match        72.9%;  Score 544; DB 2;  Length 123;
Best Local Similarity 82.6%; Pred. No. 4.6e-48;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy  20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         :||| |||||:|||||||||||||||||||||||| |:|||:| :|||||||||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy  80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         |||||| |||||||||:||:||:||| ||||||||:|||||||||||||||||||||| |
Db  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy 140 V 140
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Db 121 V 121

RESULT 15
PCT-US95-01219-11
; Sequence 11, Application PC/TUS9501219
; GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
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;  SEQUENCE CHARACTERISTICS:
;     LENGTH:  123 amino acids
;     TYPE:    amino acid
;     STRANDEDNESS: single
;     TOPOLOGY:  linear
;     MOLECULE TYPE: protein
PCT-US95-01219-11
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Query Match         72.9%;  Score 544;  DB 5;  Length 123;
Best Local Similarity  82.6%;  Pred. No. 4.6e-48;
Matches 100;  Conservative  11;  Mismatches  10;  Indels  0;  Gaps  0;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          :||| ||||| ||||||:|| ||||||||||| |:| | |||:|||||||||||||
Db    1 QVQLVQSGGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
          ||||: |||||::|||::||| |||||||:|||||||||||||||||||||| ||
Db   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy  140 V 140
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Db  121 V 121
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Search completed: January  6, 2003, 13:19:08
Job time : 12.596 secs
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 6, 2003, 13:17:36 ; Search time 6.78788 Seconds
(without alignments)
390.875 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	491.5	65.9	255	10	US-09-910-059-19	Sequence 19, Appl
2	488.5	65.5	136	10	US-09-564-329A-11	Sequence 11, Appl
3	488.5	65.5	136	10	US-09-855-153-11	Sequence 11, Appl
4	488.5	65.5	136	10	US-09-854-811-11	Sequence 11, Appl
5	488.5	65.5	136	10	US-09-934-773-11	Sequence 11, Appl
6	488.5	65.5	136	10	US-09-963-620-11	Sequence 11, Appli
7	483.5	64.8	139	10	US-09-809-739-5	Sequence 5, Appli
8	475.5	63.7	535	9	US-09-968-851-38	Sequence 38, Appl
9	475	63.7	117	10	US-09-158-120A-18	Sequence 18, Appli
10	473.5	63.5	153	10	US-09-861-294-4	Sequence 4, Appli
11	467.5	62.7	112	9	US-10-032-482-7	Sequence 7, Appli
12	466.5	62.5	120	10	US-09-910-059-11	Sequence 11, Appl
13	461	61.8	117	10	US-09-976-787-23	Sequence 23, Appl
14	461	61.8	117	10	US-09-865-198-22	Sequence 22, Appl
15	461	61.8	238	10	US-09-976-787-29	Sequence 29, Appli
16	461	61.8	238	10	US-09-865-198-28	Sequence 28, Appl
17	460	61.7	117	10	US-09-976-787-7	Sequence 7, Appli
18	460	61.7	117	10	US-09-865-198-7	Sequence 7, Appli
19	460	61.7	240	10	US-09-976-787-28	Sequence 28, Appl
20	460	61.7	240	10	US-09-865-198-27	Sequence 27, Appl
21	457	61.3	138	10	US-09-753-436-78	Sequence 78, Appl
22	455	61.0	140	10	US-09-748-960-4	Sequence 4, Appli
23	451.5	60.5	139	12	US-10-006-773-13	Sequence 13, Appl
24	447	59.9	143	1	US-08-779-784-26	Sequence 26, Appl
25	442	59.2	136	9	US-09-956-206A-47	Sequence 47, Appl
26	442	59.2	180	10	US-09-748-960-6	Sequence 6, Appli
27	440.5	59.0	124	9	US-09-974-052-1	Sequence 1, Appli
28	440.5	59.0	124	9	US-09-974-051-1	Sequence 1, Appli
29	438	58.7	136	9	US-09-956-206A-63	Sequence 63, Appl
30	424.5	56.9	252	10	US-09-971-543-1	Sequence 1, Appli
31	423.5	56.8	244	10	US-09-940-391-1	Sequence 1, Appli
32	422.5	56.6	127	10	US-09-998-831-7	Sequence 7, Appli
33	421	56.4	470	10	US-09-859-053-28	Sequence 28, Appl
34	420.5	56.4	120	10	US-09-971-543-11	Sequence 11, Appl
35	419.5	56.2	249	10	US-09-984-186-18	Sequence 18, Appl
36	415.5	55.7	122	1	US-08-779-784-28	Sequence 28, Appl
37	415.5	55.7	139	10	US-09-760-723-8	Sequence 8, Appli
38	415.5	55.7	139	10	US-09-355-925-8	Sequence 8, Appli
39	415	55.6	117	10	US-09-158-120A-17	Sequence 17, Appl
40	414	55.5	138	1	US-08-779-784-31	Sequence 31, Appl
41	412.5	55.3	139	10	US-09-760-723-7	Sequence 7, Appli
42	412.5	55.3	139	10	US-09-355-925-7	Sequence 7, Appli
43	412	55.2	142	10	US-09-772-120-8	Sequence 8, Appli
44	410.5	55.0	137	10	US-09-753-436-43	Sequence 43, Appl
45	405	54.3	230	10	US-09-995-693-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-910-059-19
; Sequence 19, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 19
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric HuIgG2 Fd construct
US-09-910-059-19

Query Match   65.9%; Score 491.5; DB 10; Length 255;
Best Local Similarity 71.5%; Pred. No. 6.2e-32;
Matches 98; Conservative 13; Mismatches 21; Indels 5; Gaps 2;

Qy   4 SWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQG 63
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Db   6 NWI--FLVTLLNGIQCEVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQG 63

Qy   64 LEWIGRIDPANGYTKYDPKFQGKATTADTSSNTAVIQLSSLTSEDTAVYFCAREGYYGN 123
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Db   64 LEWIAWIDPENGDTEYAPKFRGKATLTADSSNTAYLHLSSLTSEDTAVYYCHVLIY--- 120

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Qy    124 YGVYAMDYWGQGTSVTV 140
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Db    121 AGYLAMDYWGQGTSVAV 137
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RESULT 2
US-09-564-329A-11
; Sequence 11, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54USI4
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 136
;   TYPE: PRT
;   ORGANISM: SCID Mice
US-09-564-329A-11

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Query Match             65.5%;      Score 488.5;  DB 10;   Length 136;
Best Local Similarity   74.4%;      Pred. No. 5.8e-32;
Matches   99; Conservative   7; Mismatches   16;  Indels   11;  Gaps   1;

Qy    8  FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
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Db    2  FFLMAVVIGVNSEVQLQQSGAELVRSGASVKLSCTASGFNIKDYIHWVNQRPDQGLEWI 61

Qy    68 GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
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Db    62 GWIDPENGDTEFVPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGG-------- 113

Qy    128 AMDYWGQGTSVTV 140
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Db    114 ---FWGQGTLVTV 123
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RESULT 3
US-09-855-153-11
; Sequence 11, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54USI4
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 136
;   TYPE: PRT
;   ORGANISM: SCID Mice
US-09-855-153-11

```
Query Match             65.5%;      Score 488.5;  DB 10;   Length 136;
Best Local Similarity   74.4%;      Pred. No. 5.8e-32;
Matches   99; Conservative   7; Mismatches   16;  Indels   11;  Gaps   1;

Qy    8  FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
         |||||| |||||||||||||||||||||||||||||| ||| ||| :||||||||
Db    2  FFLMAVVIGVNSEVQLQQSGAELVRSGASVKLSCTASGFNIKDYIHWVNQRPDQGLEWI 61

Qy    68 GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
         | ||| || | | :::  |||||| |:::  ||||| ||:||||||||||||;:  |
Db    62 GWIDPENGDTEFVPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGG-------- 113

Qy    128 AMDYWGQGTSVTV 140
          :|||| |||
Db    114 ---FWGQGTLVTV 123
```

RESULT 4
US-09-854-811-11
; Sequence 11, Application US/09854811
; Patent No. US2002011957A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54USI4
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 136

```
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-11

Query Match     65.5%;   Score 488.5;  DB 10;   Length 136;
Best Local Similarity   74.4%;   Pred. No. 5.8e-32;
Matches   99;  Conservative   7;  Mismatches   16;  Indels   11;  Gaps   1;

Qy    8  FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
         |||||| ||||||||||||||||||:|||||||||||||||||| | |||::|||||
Db    2  FFLMAVVIGVNSEVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWI 61

Qy   68  GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
         | ||| || ||:: |||||||||:||| ||||| |||||||||||||||::|||:|
Db   62  GWIDPENGDTEFVPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGG-------- 113

Qy  128  AMDYWGQGTSVTV 140
         :||||| |||
Db  114  ---FWGQGTLVTV 123
```

RESULT 5
US-09-934-773-11
; Sequence 11, Application US/09934773
; Patent No. US2002013668A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-11

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Query Match     65.5%;   Score 488.5;  DB 10;   Length 136;
Best Local Similarity   74.4%;   Pred. No. 5.8e-32;
Matches   99;  Conservative   7;  Mismatches   16;  Indels   11;  Gaps   1;

Qy    8  FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
         |||||| ||||||||||||||||||:|||||||||||||||||| | |||::|||||
Db    2  FFLMAVVIGVNSEVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWI 61

Qy   68  GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
         | ||| || ||:: |||||||||:||| ||||| |||||||||||||||::|||:|
Db   62  GWIDPENGDTEFVPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGG-------- 113

Qy  128  AMDYWGQGTSVTV 140
         :||||| |||
Db  114  ---FWGQGTLVTV 123
```

RESULT 6
US-09-963-620-11
; Sequence 11, Application US/09963620
; Patent No. US2002014194IA1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-963-620-11

```
Query Match     65.5%;   Score 488.5;  DB 10;   Length 136;
Best Local Similarity   74.4%;   Pred. No. 5.8e-32;
Matches   99;  Conservative   7;  Mismatches   16;  Indels   11;  Gaps   1;

Qy    8  FFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWI 67
         |||||| ||||||||||||||||||:|||||||||||||||||| | |||::|||||
Db    2  FFLMAVVIGVNSEVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWI 61

Qy   68  GRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVY 127
         | ||| || ||:: |||||||||:||| ||||| |||||||||||||||::|||:|
Db   62  GWIDPENGDTEFVPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTGG-------- 113

Qy  128  AMDYWGQGTSVTV 140
         :||||| |||
Db  114  ---FWGQGTLVTV 123
```

RESULT 7
US-09-809-739-5
; Sequence 5, Application US/09809739

; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
;   Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 5
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)...(139)
;   OTHER INFORMATION: YFC51.1 heavy chain variable region
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(19)
;   OTHER INFORMATION: Rat
US-09-809-739-5

Query Match   64.8%; Score 483.5; DB 10; Length 139;
Best Local Similarity 66.7%; Pred. No. 1.5e-31;
Matches 94; Conservative 16; Mismatches 26; Indels 5; Gaps 2;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP   60
            ||||: |||: || :||||||| |::||||||| |||||||||| :| ||| ||
Db   1 MKCSWINLFLMALASGVTAEVQLQQSGPELRRPGSSVKLSCKTSGYSIKDYLLHWVKHRP   60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            ||||||||| ||| :||||| :||:|||||||||||||||||||:||| | |
Db   61 EYGLEWIGWIDPEGETKYGQKFQSRATLTADTSSNTAYMQLSSLTSDDTATYFCTRGEY 120

Qy 121 -YGNYGVYAMDYWGQGTSVTV 140
            ||||| |||:|||||
Db 121 RYNSW---FDYWGQGTLVTV 137

RESULT 8
US-09-968-851-38
; Sequence 38, Application US/09968851
; Publication No US20020193561A1
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
;   BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
;   USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
;   DUNNER, LLP
;   STREET: 1300 I Street, NW
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005-3315
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/968,851
;   FILING DATE: 03-Oct-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/983,035
;   FILING DATE: 20-Feb-1998

;   APPLICATION NUMBER: PCT/FR96/01111
;   FILING DATE: 17-JUL-1996
;   APPLICATION NUMBER: FR 95/08729
;   FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Strauss, William L.
;   REGISTRATION NUMBER: 47,114
;   REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-408-4000
;   TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 535 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38

Query Match   63.7%; Score 475.5; DB 9; Length 535;
Best Local Similarity 77.0%; Pred. No. 2.2e-30;
Matches 94; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

Qy   19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK   78
            ::||||||||||||||||||||||||||||| |:|:| :||||||||| |||:|||
Db   2 AQVQLQESGAELVGSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTE   61

Qy   79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
           :|||||||| ||||||||||||||||| |||||| | ||: : ||| |||||||||
Db   62 YAPKFQGKAIMTADTSSNTAYLQLSSLASEDTAVYC----NFYGD----ALDYWGQGTTV 114

Qy 139 TV 140
           ||
Db 115 TV 116

RESULT 9
US-09-158-120A-18
; Sequence 18, Application US/09158120A
; Patent No. US20020102257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
;   Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;   STEWART & OLSTEIN
;   STREET: 6 BECKER FARM ROAD
;   CITY: ROSELAND
;   STATE: NEW JERSEY
;   COUNTRY: USA
;   ZIP: 07068
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: P160
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: MS Word 97
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/158,120A
;   FILING DATE: September 21, 1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/290,592
;   FILING DATE: August 15, 1994
;   APPLICATION NUMBER: 07/813,372
;   FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Olstein, Elliot M.
;   REGISTRATION NUMBER: 24,025
;   REFERENCE/DOCKET NUMBER: 469201-367
; TELECOMMUNICATION INFORMATION:

```
;       TELEPHONE:  973-994-1700
;       TELEFAX:    973-994-1744
;   INFORMATION FOR SEQ ID NO:  18:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH:  117 AMINO ACIDS
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;       MOLECULE TYPE:  PROTEIN
US-09-158-120A-18

Query Match             63.7%;  Score 475;  DB 10;  Length 117;
Best Local Similarity   76.9%;  Pred. No. 5.7e-31;
Matches    93;  Conservative   10;  Mismatches   12;  Indels    6;  Gaps    1;

Qy     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          ||||||||||||:|| ||||||| |||||| |:: |||||||||||||||| : |||
Db      1 EVQLQQSGAELVRPGALVKLSCKASGFNIKDYIYWVKQRPEQGLEWIGWIDPENGNTVF 60

Qy     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
          ||||||:||:||||||||||||||||||||||||||   || : ||||||::|
Db     61 DPKFQGKASITSDTSSNTAYLQLSSLTSEDTAVYYCA------YYGTSSFDFWGQGTTLT 114

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
             |:|||||||||||
Db    115 V                   115
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RESULT 10
US-09-861-294-4
; Sequence 4, Application US/09861294
; Patent No. US2002009819OA1
; GENERAL INFORMATION:
;   APPLICANT: Malaya CHATTERJEE
;   APPLICANT: Kenneth A. FOON
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;   TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
;   FILE REFERENCE: 30414200062O
;   CURRENT APPLICATION NUMBER: US/09/861,294
;   CURRENT FILING DATE: 2001-05-17
;   PRIOR APPLICATION NUMBER: 60/049,540
;   PRIOR FILING DATE: 1997-06-13
;   PRIOR APPLICATION NUMBER: 09/096,244
;   PRIOR FILING DATE: 1998-06-11
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(19)
US-09-861-294-4

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Query Match             63.5%;  Score 473.5;  DB 10;  Length 153;
Best Local Similarity   64.3%;  Pred. No. 9.7e-31;
Matches    90;  Conservative   21;  Mismatches   24;  Indels    5;  Gaps    1;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||: |||| ||:::| ||:::: :||||| | |||||||||||||||||:
Db      1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCCKASGYTLTSYNMHWVKQTP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||||| | || ||||| :|||||||||:|:|:|||||||||:|||||||:||||||
Db     61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
             |:||||||||||||
Db    121 EG----ALDYWGQGTSVTV 135
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RESULT 11
US-10-032-482-7

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; Sequence 7, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
;   APPLICANT:  Cohen, Irun
;   APPLICANT:  ROTTER, Varda
;   APPLICANT:  Wolkowicz, Roland
;   APPLICANT:  RUIZ, Pedro
;   APPLICANT:  EREZ-ALON, Neta
;   APPLICANT:  HERKEL, Johannes
;   TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
;   TITLE OF INVENTION:  IMMUNITY
;   FILE REFERENCE: COHEN42
;   CURRENT APPLICATION NUMBER: US/10/032,482
;   CURRENT FILING DATE:  2002-01-02
;   PRIOR APPLICATION NUMBER: US/09/445,602
;   PRIOR FILING DATE:  2001-01-24
;   PRIOR APPLICATION NUMBER: PCT/IL98/00266
;   PRIOR FILING DATE:  1999-12-09
;   PRIOR APPLICATION NUMBER: IL 121041
;   PRIOR FILING DATE:  1997-06-09
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-032-482-7

Query Match             62.7%;  Score 467.5;  DB 9;  Length 112;
Best Local Similarity   78.0%;  Pred. No. 2.1e-30;
Matches    92;  Conservative   10;  Mismatches    9;  Indels    7;  Gaps    2;

Qy     23 LQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPK 82
          |:||||||| :|:|||||||:||||||||||:|: | |||||||||||||| ||| |||
Db      1 LQESGAELVRSGASVKLSCIASGFNIKDYIMHWVKQRPEQGLEWIGWIDPENGDTEYAPK 60

Qy     83 FQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
          |||||:|||||||||||||||||||||||:||:    :||:  :|:|||||||||:|||
Db     61 FQGKATMTADTSSNTAYLQLSSLASEDTAVYYC---NFYGD---ALDYWGQGTVVTV 111
```

RESULT 12
US-09-910-059-11
; Sequence 11, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
;   APPLICANT: Copley, Clive G
;   APPLICANT: Edge, Michael Derek
;   APPLICANT: Emery, Stephen Charles
;   TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
;   TITLE OF INVENTION: Their Therapeutic use in an Adept System
;   FILE REFERENCE: 1991-209
;   CURRENT APPLICATION NUMBER: US/09/910,059
;   CURRENT FILING DATE: 2001-07-23
;   PRIOR APPLICATION NUMBER: US 09/171,945
;   PRIOR FILING DATE: 1998-10-29
;   PRIOR APPLICATION NUMBER: PCT/GB97/01165
;   PRIOR FILING DATE: 1997-04-29
;   PRIOR APPLICATION NUMBER: GB 9703103.3
;   PRIOR FILING DATE: 1997-02-14
;   PRIOR APPLICATION NUMBER: GB9609405.7
;   PRIOR FILING DATE: 1996-05-04
;   NUMBER OF SEQ ID NOS: 131
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-910-059-11

Query Match   62.5%; Score 466.5; DB 10; Length 120;
Best Local Similarity   77.7%; Pred. No. 2.7e-30;
Matches   94; Conservative   7; Mismatches   17; Indels   3; Gaps   1;
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```
Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
           |||||||||| |||||||||:|| |:||||||||||||||||||| ||| :|
Db    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY  60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           ||:|||:|||:||||||||||||||||||||:|    |||||||
Db   61 APKFRGKATLTADSSNTAYLHLSSLTSEDTAVYYCHVLIY---AGYLAMDYWGQGTSVA 117

Qy  140 V 140
          |
Db  118 V 118
```

RESULT 13
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US2002006452BA1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

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Query Match             61.8%;  Score 461;  DB 10;  Length 117;
Best Local Similarity   76.0%;  Pred. No. 7.1e-30;
Matches  92;  Conservative   9;  Mismatches  14;  Indels   6;  Gaps   2;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
           :|:||||||| ||||||||||||||||||||||| ::|  |:|
Db    1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY  60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTTVT 139
           ||||||||||||  ||:|||:||:|||||||||||:|     |||||:||
Db   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDY----EGYWGQGTTVT 114

Qy  140 V 140
          |
Db  115 V 115
```

RESULT 14
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US2002010334BA1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Method
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse

US-09-865-198-22

```
Query Match             61.8%;  Score 461;  DB 10;  Length 117;
Best Local Similarity   76.0%;  Pred. No. 7.1e-30;
Matches  92;  Conservative   9;  Mismatches  14;  Indels   6;  Gaps   2;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
           :|:||||||| ||||||||||||||||||||||| ::|  |:|
Db    1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY  60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           ||||||||||| ||:|||:||:|||||||||||:|     |||:|
Db   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDY----EGYWGQGTTVT 114

Qy  140 V 140
          |
Db  115 V 115
```

RESULT 15
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US2002006452BA1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

```
Query Match             61.8%;  Score 461;  DB 10;  Length 238;
Best Local Similarity   76.0%;  Pred. No. 1.4e-29;
Matches  92;  Conservative   9;  Mismatches  14;  Indels   6;  Gaps   2;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
           :|:||||||| ||||||||||||||||||||||| ::|  |:|
Db    1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY  60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           ||||||||||| ||:|||:||:|||||||||||:|     |||:|
Db   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDY----EGYWGQGTTVT 114

Qy  140 V 140
          |
Db  115 V 115
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Search completed: January 6, 2003, 13:29:31
Job time : 7.78788 secs

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                GenCore version 5.1.3
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    January  6, 2003, 13:12:26 ; Search time 13.0101 Seconds
                                        (without alignments)
                                        1034.490 Million cell updates/sec

Title:      US-09-155-739-4
Perfect score: 746
Sequence:   1 MKCSWVMFFLMAVVTGVNSE..........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_73:*
            1:  pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	603.5	80.9	178	2	S29594	Ig gamma chain (WM
2	597	80.0	136	2	S04576	Ig heavy chain pre
3	570.5	76.5	137	2	S52445	Ig heavy chain V r
4	567.5	76.1	123	2	PH1403	Ig heavy chain V r
5	539	72.3	120	2	S03471	Ig heavy chain V-D
6	523	70.1	117	2	S17586	Ig heavy chain V r
7	521.5	69.9	122	2	S06823	Ig heavy chain V r
8	515	69.0	115	2	S03482	Ig heavy chain V-D
9	500	67.0	116	2	S24289	Ig gamma chain V r
10	498	66.8	120	2	S03484	Ig heavy chain V-D
11	494.5	66.3	120	2	A56446	Ig heavy chain V r
12	493.5	66.2	268	2	PH1012	Ig heavy chain V r
13	492	66.0	108	2	S49220	Ig gamma-1 chain -
14	472.5	63.3	221	4	A47271	nitrophenyl phosph
15	471	63.1	114	2	PH1482	Ig heavy chain V r
16	467	62.6	107	2	PH1013	Ig heavy chain V r
17	466.5	62.5	139	2	PS0024	Ig heavy chain pre
18	464.5	62.3	139	1	MHMS18	Ig heavy chain pre
19	462.5	62.0	99	2	D37262	Ig heavy chain V r
20	461.5	61.9	115	2	PL0246	Ig heavy chain V r
21	461.5	61.9	139	2	A27609	Ig heavy chain pre
22	460.5	61.7	141	2	JL0076	Ig heavy chain pre
23	459	61.5	135	2	PH1492	Ig heavy chain V r
24	459	61.5	140	1	HVMSG7	Ig heavy chain pre
25	457.5	61.3	107	2	A27646	Ig heavy chain pre
26	457	61.3	138	2	E32513	Ig heavy chain pre
27	456	61.1	249	2	S41374	single chain Fv an
28	455.5	61.1	141	2	A39276	Ig heavy chain pre
29	455	61.0	140	2	PH1498	Ig heavy chain V r
30	454.5	60.9	133	2	PC1155	Ig heavy chain pre
31	454	60.9	118	2	S25174	Ig heavy chain V r
32	454	60.9	138	2	S21810	Ig heavy chain V r
33	453	60.7	140	2	PH1484	Ig heavy chain V r
34	452	60.6	135	2	PH1493	Ig heavy chain V r
35	451.5	60.5	469	2	S37483	Ig gamma-2a chain
36	451	60.5	135	2	PH1494	Ig heavy chain V r
37	447	59.9	140	2	PH1489	Ig heavy chain V r
38	444	59.5	140	2	PH1486	Ig heavy chain V r
39	441	59.1	140	2	PH1488	Ig heavy chain V r
40	440.5	59.0	120	2	S41394	Ig heavy chain V r
41	440	59.0	122	2	S20643	Ig gamma chain - m
42	440	59.0	246	2	S38950	Ig gamma-2a chain
43	440	59.0	446	2	S40295	Ig gamma-2a chain
44	439	58.8	123	2	S20646	Ig heavy chain V r
45	438	58.7	99	2	C37262	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
  submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEV>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match             80.9%;  Score 603.5;  DB 2;  Length 178;
Best Local Similarity   88.1%;  Pred. No. 2.1e-45;
Matches 118;  Conservative  6;  Mismatches  5;  Indels  5;  Gaps  2;

Qy     7 MFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEW 66
           :|||||||||||||||||||||||||||||||||||||||||||:  ||||:|||:||||
Db     1 IFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEW 60

Qy    67 IGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGV 126
          |||||||||||| ||||||||||||||||| |||||||||||||||||| |
Db    61 IGRIDPANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG---GNY-A 115

Qy   127 YAMDYWGQGTSVTV 140
          | ||||||||||||
Db   116 YGMDYWGQGTSVTV 129


RESULT 2
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
  Eur.J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involv
A;Reference number: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
```

Query Match   80.0%;   Score 597; DB 2;   Length 136;
Best Local Similarity   82.9%;   Pred. No. 5.9e-45;
Matches 116; Conservative   6; Mismatches   12; Indels   6; Gaps   1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||||:|||||||| |||||||||||||||||||::||||||||||||||||:| |||||
Db   1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||||||| ||| ||:| |||||||||||||||||||||||||||:||
Db   61 EQGLEWIGWIDPENGDTQYASKFQGKATMTADTSSNTTYIQLSSLTSEDTAVYYCT---- 116

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
          ||||||||||||||||||
Db   117 --TYGAYAMDYWGQGTSVTV 134

RESULT 3
S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
A;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match   76.5%;   Score 570.5; DB 2;   Length 137;
Best Local Similarity   81.4%;   Pred. No. 1.2e-42;
Matches 114; Conservative   6; Mismatches   15; Indels   5; Gaps   2;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||||:|||||||| ||||||||||||||| |:||||||||||||||||::| |||||
Db   1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDDYMYWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||||||| ||| ||:| |||||||||||||||:||:|| |
Db   61 EQGLEWIGWIDPENGTNVYDPKFQGKASTTADTSSNTTYIQLSSLASEDTAVYYCA---Y 117

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
          || |||||||||||||
Db   118 YGT--SYWFPYWGQGTLVTV 135

RESULT 4
PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000.
C;Accession: PH1403
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A;Reference number: PH1403; MUID:93018837; PMID:1402663
A;Accession: PH1403
A;Molecule type: DNA
A;Residues: 1-123 <SHI>
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

---

C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>

Query Match   76.1%;   Score 567.5; DB 2;   Length 123;
Best Local Similarity   94.9%;   Pred. No. 1.9e-42;
Matches 111; Conservative   3; Mismatches   2; Indels   1; Gaps   1;

Qy   1 MKCSWVMFFLMAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
          ||||||:|||||||| |:|||||||||||||||||||||||||||||||||||:|||||||
Db   1 MKCSWVIFFLMAVVTAGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQR 60

Qy   60 PEQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||:|:|
Db   61 PEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA 117

RESULT 5
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.3%;   Score 539; DB 2;   Length 120;
Best Local Similarity   89.3%;   Pred. No. 5.6e-40;
Matches 108; Conservative   2; Mismatches   2; Indels   7; Gaps   1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          |||||||||||||||||||||||||||||||||||:|||||||||||||||||||| ||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
          ||||||||||||||||||||||||||||||||||:|:|| |||||||||||||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR---------GWLRRDAMDYWGQGTSVT 116

Qy   140 V 140
          |
Db   117 V 117

RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
forms.
A;Reference number: S17586; MUID:92015240; PMID:1656053
A;Accession: S17586
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL.X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   70.1%; Score 523; DB 2; Length 117;
Best Local Similarity 85.2%; Pred. No. 1.4e-38;
Matches 104; Conservative 7; Mismatches 3; Indels 8; Gaps 3;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||:|||||||||||||||||:| |||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy    80 DPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYFCAREGY-YGNYGVYAMDYWGQGTSV 138
         |||| |||||||||||||||||||||||||||||::|    |||||::
Db    61 DPKFQDKATTADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy   139 TV 140
         ||
Db   114 TV 115
```

RESULT 7
S06823
Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match   69.9%; Score 521.5; DB 2; Length 122;
Best Local Similarity 86.9%; Pred. No. 1.9e-38;
Matches 106; Conservative 4; Mismatches 4; Indels 9; Gaps 3;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIH-CVKQRPEQGLEWIGRIDPANGYTK 78
         ||||||||||||||||||||||||||||||||||:| |||||||||||||||||:| |||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy    79 YDPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
         |||||||||||||||||||||||||||||||||||:|    :||||||
Db    61 YDPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy   139 TV 140
         ||
Db   119 TV 120
```

RESULT 8
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
A;Variety: strain BALB/c
C;Accession: S03482; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL.X03219
A;Note: this sequence was determined from the differentiated gene
;R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   69.0%; Score 515; DB 2; Length 115;
Best Local Similarity 83.5%; Pred. No. 6.6e-38;
Matches 101; Conservative 4; Mismatches 10; Indels 6; Gaps 1;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||:| |||||||||||||||:| |||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy    80 DPKFQGKATTADTSSNTAYLQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 139
         |||||||||||||||||||||||||||||||:||       |||||::|
Db    61 DPKFQGKATITTDTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114

Qy   140 V 140
         |
Db   115 V 115
```

RESULT 9
S24289
Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL.X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match   67.0%; Score 500; DB 2; Length 116;
Best Local Similarity 81.0%; Pred. No. 1.3e-36;
Matches 98; Conservative 9; Mismatches 6; Indels 8; Gaps 2;

```
Qy    21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
         |||||||||||||||||||||||||||||||||:| ||||||||||||||||:|
Db     1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy    81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EGYGNYGVYAMDYWGQGTSVT 139
         |||||||||||||||||||||||||||||||||| ||        |||||::
Db    61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY------FDYWGQGTTLT 113

Qy   140 V 140
         |
Db   114 V 114
```

RESULT 10
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c

C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   66.8%;   Score 498; DB 2; Length 120;
Best Local Similarity 82.6%;   Pred. No. 2.1e-36;
Matches 100; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||| |||||||||||||||||||:| ||||||||||||||||||    ||
Db     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60

Qy    80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         |||||||||||||||:|   :||||||| |||||||:|        ||||||||||||||
Db    61 GPKFQGKATITADTSSSSAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy   139 TV 140
          | |
Db   117 TV 118
```

RESULT 11
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match   66.3%;   Score 494.5; DB 2; Length 268;
Best Local Similarity 80.3%;   Pred. No. 9.5e-36;
Matches 98; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

```
Qy    19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK 78
         :||:|:|||||||||||||||||||:|||||||| |||| |||||||||||||| ||| ||
Db     2 AQVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITK 61

Qy    79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
         |||||||||||| ||||||||||||||||||||||:|         :||||||||||||:
Db    62 YDPKFQGKATITAADTSSNTAYLQLSSLTSEDTAVYYCA-SYYLTRY---ENYWGQGTTV 116

Qy   139 TV 140
          | |
Db   117 TV 118
```

RESULT 12
PH1012
Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1012
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   66.2%;   Score 493.5; DB 2; Length 108;
Best Local Similarity 85.8%;   Pred. No. 4.6e-36;
Matches 97; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||| ||||||||||||||||| :| ||||||||||||||||||||||:||
Db     1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy    80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYW 132
         ||| ||||||||||||||||||||||||||||:||||||||  :----YAMDYW
Db    61 APKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCARRDNY-----YAMDYW 108
```

RESULT 13
S49220
Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match   66.0%;   Score 492; DB 2; Length 221;
Best Local Similarity 79.3%;   Pred. No. 1.3e-35;
Matches 96; Conservative 8; Mismatches 13; Indels 4; Gaps 1;

```
Qy    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         :| :|||||||||| |||||||||||||||||| :| ||||||||||||||||| ::||
Db     1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy    80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         |||||| ||||||||:||||||||||||||||||:||  |    | ::---YGWGQGTTLT
Db    61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116

Qy   140 V 140
           |
Db   117 V 117
```

RESULT 14

A47271
nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C;Accession: A47271
R;Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic acti
A;Reference number: A47271; MUID:9316560; PMID:8094556
A;Accession: A47271
A;Molecule type: DNA; protein
A;Residues: 1-114 <LES>
A;Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A;Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted

Query Match   63.3%;   Score 472.5; DB 4;   Length 114;
Best Local Similarity   77.7%;   Pred. No. 3.2e-34;
Matches   94; Conservative   8; Mismatches 10; Indels   9; Gaps   2;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         :|:| :||||||||||||||||||||||: |:|||:||:||||||||||||||||| ||
Db   1 QVKLLESGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKY 60

Qy   80 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         |||| ||||||||||||||||:||||||||||||||||| ||||||::||
Db   61 DPKFQDKATITADTSSKTTYIQLSGLTSEDTAVYYCA--SYYG------IYWGQGTTLT 111

Qy   140 V 140
         |
Db   112 V 112

RESULT 15
PH1482
Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1482
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   63.1%;   Score 471; DB 2;   Length 140;
Best Local Similarity   65.0%;   Pred. No. 5.4e-34;
Matches   91; Conservative 19; Mismatches 28; Indels   2; Gaps   1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         |: : ||::| ||:||||||||||| |:|||||:|||:||||||: |: ||||||||||
Db   1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGY 120
         | ||||||||| :|:| |: ||:|| :|||| |:||| : :|| ||||:|||||| |:||
Db   61 GQGLEWIGYINPGNGYTKYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVY 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
         || | |||||||||||:||
Db   121 YG--GSYYFDYWGQGTTLTV 138

```
                    GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:        January  6, 2003, 12:48:25 ; Search time 7.07071 Seconds
                                (without alignments)
                                821.231 Million cell updates/sec

Title:          US-09-155-739-4
Perfect score:  746
Sequence:       1 MKCSWVMFFLMAVVTGVNSE..........YGNYGVYAMDYWGQGTSVTV 140

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:       112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_40:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                %
Result          Query
No.    Score   Match Length DB  ID              Description
----   -----   ----- ------ --  --              -----------
  1    464.5   62.3    139   1  HV07_MOUSE      P01751 mus musculu
  2    459     61.5    140   1  HV02_MOUSE      P01746 mus musculu
  3    425     57.0    120   1  HV03_MOUSE      P01747 mus musculu
  4    422.5   56.6    137   1  HV11_MOUSE      P01755 mus musculu
  5    416     55.8    138   1  HV48_MOUSE      P03980 mus musculu
  6    411     55.1    117   1  HV09_MOUSE      P01753 mus musculu
  7    396     53.1    136   1  HV15_MOUSE      P01759 mus musculu
  8    393     52.7    117   1  HV06_MOUSE      P01750 mus musculu
  9    393     52.7    117   1  HV49_MOUSE      P06328 mus musculu
 10    389     52.1    117   1  HV04_MOUSE      P01754 mus musculu
 11    388     52.0    117   1  HV52_MOUSE      P06327 mus musculu
 12    381     51.1    117   1  HV13_MOUSE      P01757 mus musculu
 13    379     50.8    121   1  HV01_MOUSE      P01745 mus musculu
 14    379     50.8    147   1  HV1C_HUMAN      P01744 homo sapien
 15    378.5   50.7    117   1  HV05_MOUSE      P01749 mus musculu
 16    374     50.1    117   1  HV12_MOUSE      P01756 mus musculu
 17    374     50.1    117   1  HV14_MOUSE      P01758 mus musculu
 18    372     49.9    118   1  HV51_HUMAN      P06330 homo sapien
 19    368.5   49.4    117   1  HV1B_HUMAN      P01743 homo sapien
 20    367     49.2    120   1  HV50_MOUSE      P06329 mus musculu
 21    360.5   48.3    117   1  HV1G_HUMAN      P23083 homo sapien
 22    359     48.1    136   1  HV16_MOUSE      P01783 mus musculu
 23    356.5   47.8    114   1  HV00_MOUSE      P01741 mus musculu
 24    321.5   43.1    119   1  HV38_MOUSE      P01808 mus musculu
 25    316.5   42.4    117   1  HV42_MOUSE      P01812 mus musculu
 26    315     42.2    117   1  HV1A_HUMAN      P01742 homo sapien
 27    314     42.1    119   1  HV37_MOUSE      P01807 mus musculu
 28    312.5   41.9    142   1  HV01_RAT        P01805 rattus norv
 29    311     41.7    119   1  HV40_MOUSE      P01810 mus musculu
 30    310.5   41.6    118   1  HV39_MOUSE      P01809 mus musculu
 31    304     40.8    137   1  HV46_MOUSE      P01822 mus musculu
 32    297     39.8    144   1  HV26_MOUSE      P01795 mus musculu
 33    297     39.8         1
```

```
 34    293.5   39.3   120   1  HV1H_HUMAN       P80421 homo sapien
 35    292     39.1   117   1  HV41_MOUSE       P01811 mus musculu
 36    291.5   39.1   116   1  HV05_CARAU       P19181 carassius a
 37    290     38.9   116   1  HV36_MOUSE       P01806 mus musculu
 38    290     38.9   123   1  HV24_MOUSE       P01793 mus musculu
 39    288     38.6   117   1  HV3C_HUMAN       P01764 homo sapien
 40    285.5   38.3   116   1  HV3T_HUMAN       P01781 homo sapien
 41    284.5   38.1   122   1  HV3G_HUMAN       P01768 homo sapien
 42    284     38.1   144   1  HV43_MOUSE       P01819 mus musculu
 43    284     38.1   146   1  HV2I_HUMAN       P06331 homo sapien
 44    282.5   37.9   122   1  HV3A_HUMAN       P01762 homo sapien
 45    282     37.8   125   1  HV1F_HUMAN       P06326 homo sapien

                                ALIGNMENTS

RESULT 1
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;    139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the Npb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   --------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC       or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MIMS18.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    139                 IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN       20     49                 FRAMEWORK-1.
FT   DOMAIN       50     54                 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68                 FRAMEWORK-2.
FT   DOMAIN       69     85                 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117                 FRAMEWORK-3.
FT   DOMAIN      118    124                 D SEGMENT.
FT   DOMAIN      125    139                 JH2 SEGMENT.
FT   DISULFID     41    115                 BY SIMILARITY.
FT   NON_TER     139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;

     Query Match             62.3%;  Score 464.5; DB 1;  Length 139;
     Best Local Similarity   65.0%;  Pred. No. 5.7e-38;
```

```
Matches   91;  Conservative   18;  Mismatches   28;  Indels    3;  Gaps    1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | :| :|| :||  ||||||| ||||||||||||||  ||:  ::|  |||||
Db    1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           :|||||||||||||| |: ||||||: |||:  ||:|||||||||:|||:|||| |
Db   61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
           ||:  ||||||||||| :||
Db  121 YGS--SYFDYWGQGTTLTV 137

RESULT 2
HV02_MOUSE
ID   HV02_MOUSE    STANDARD;    PRT;    140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL     1     19
FT   CHAIN     20    140       IG HEAVY CHAIN V REGION 93G7.
FT   NON_TER  140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;

Query Match              61.5%;  Score 459;  DB 1;  Length 140;
Best Local Similarity    63.6%;  Pred. No. 2e-37;
Matches   89;  Conservative   18;  Mismatches   31;  Indels    2;  Gaps    1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | :| :|| :||  ||||||| ||||||||||||||  ||:  ::|  |||||
Db    1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||:  || |: ||||||:  |  ||:  :||:|||||||||||:  ||||
Db   61 GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          ||:  ||||||||||| :||
Db  121 YG--GSYDFDYWGQGTPLTV 138
```

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RESULT 3
HV03_MOUSE
ID   HV03_MOUSE    STANDARD;    PRT;    120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8313846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
-!-  MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC   DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC   CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC   SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER  120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;

Query Match              57.0%;  Score 425;  DB 1;  Length 120;
Best Local Similarity    68.3%;  Pred. No. 3.1e-34;
Matches   82;  Conservative   14;  Mismatches   22;  Indels    2;  Gaps    1;

Qy   21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
          |||||||||||||||||||||| :|:|||| ||||||||||||||||||:  :|||||
Db    1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy   81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
          ||: | :||:: ||:|||||||||||:|||| ||||  :||  |||||||||||
Db   61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLTV 118

RESULT 4
HV11_MOUSE
ID   HV11_MOUSE    STANDARD;    PRT;    137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
-!-  MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC   MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC   (NPB ANTIBODIES).
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE    137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;

Query Match             56.6%;  Score 422.5;  DB 1;  Length 137;
Best Local Similarity   61.4%;  Pred. No. 6.3e-34;
  Matches   86;  Conservative  16;  Mismatches  33;  Indels   5;  Gaps   2;

Qy         1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP   60
              |||| :  : || |||::||||||| ||| |||||||||: :| | ||||
Db         1  MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYLMHWNQRP   60

Qy        61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY  120
              :||||||||| :|| |  : ||||:|:| : |||:|::||::||||||| ||
Db        61  GRGLEWIGRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-R  119

Qy       121  YGNYGVYAMDYWGQGTSVTV  140
              |-| |||||||::||
Db       120  LGRY----FDYWGQGTTLFV  135

RESULT 5
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;       PRT;    138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      128    138       FRAMEWORK-4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE    138 AA;  15576 MW;  748157E4C6907B8E CRC64;

Query Match             55.8%;  Score 416.;  DB 1;  Length 138;
Best Local Similarity   60.0%;  Pred. No. 2.7e-33;
  Matches   84;  Conservative  21;  Mismatches  29;  Indels   6;  Gaps   2;

Qy         1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP   60
              | |:::|| || :    : ||||| ||||||||||::: :|| | ||||
Db         1  MGWSYIILFLVATATDVHSQVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRP   60

Qy        61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG  119
              ||||||||  : : :|:  : ||:|: :::|||: |||:|::|::||||| || ::
Db        61  GQGLEWIGEINPNDGRSNYNEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDG  120

Qy       120  YYGNYGVYAMDYWGQGTSVT  139
              || : |||||||::||
Db       121  YYDWF-----VYWGQGTLVT  135

RESULT 6
HV09_MOUSE
ID   HV09_MOUSE     STANDARD;       PRT;    117 AA.
AC   P01753; P11271;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 186-1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; B02034; HVMS61.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 186-1.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;  12890 MW;  16191A088CB17F5A CRC64;

Query Match             55.1%;  Score 411.;  DB 1;  Length 117;
Best Local Similarity   68.4%;  Pred. No. 6.7e-33;
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Matches    80;  Conservative    15;  Mismatches    22;  Indels    0;  Gaps    0;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |||||||||| ||:|:|| ||||||||||||||||||||||||:: |||::|| ||||
Db     1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
          :||||||||| :| ||:|| ||| :|| ||||||||||:||||||||||:||||||
Db    61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR 117

RESULT 7
HV15_MOUSE
ID   HV15_MOUSE             STANDARD;      PRT;      136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region BCL1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;

Query Match             53.1%;  Score 396;  DB 1;  Length 136;
Best Local Similarity   55.7%;  Pred. No. 2.2e-31;
Matches  78;  Conservative  23;  Mismatches  33;  Indels  6;  Gaps  2;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | :||:|| ||||||:|| |||||||||||:|| ||:||||| ||: :|| |:|||
Db     1 MGWSCIIFFLVATATGVHSQVQLQQPGSEVRPGVSVKISCKGSGYTFTDYAMHWVKQSH 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          :||||||||| :| ||:|| ||| :|| |||||||||::||||||||||:|||||| |
Db    61 AKSLEWIGVISTYNGNTSYNQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--Y 118

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
          ||||   ||:|||:||| ||
Db   119 YGNY---FDYWGQGTTLTV 134

RESULT 8
HV06_MOUSE
ID   HV06_MOUSE             STANDARD;      PRT;      117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 102 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the Npb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02032; HVMS02.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117         IG HEAVY CHAIN V REGION 102.
FT   DOMAIN       20     49         FRAMEWORK-1.
FT   DOMAIN       50     54         COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68         FRAMEWORK-2.
FT   DOMAIN       69     85         COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117         FRAMEWORK-3.
FT   DISULFID     41    115         BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12867 MW;  740A65DD851FCA8C CRC64;     Length 117;

Query Match             52.7%;  Score 393;  DB 1;  Length 117;
Best Local Similarity   65.5%;  Pred. No. 3.6e-31;
Matches  76;  Conservative  17;  Mismatches  23;  Indels  0;  Gaps    0;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | : ||:|| |||:| || ||||||||||||||||||||||||||: :||:|| ||||
Db     1 MGWSCIILFLVATATGVHSHVQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRP 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
          |||||||||||||| :||:|||||||||| |||:||:|||||||||||:||| |||
Db    61 GQGLEWIGRIHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

RESULT 9
HV49_MOUSE
ID   HV49_MOUSE             STANDARD;      PRT;      117 AA.
AC   P06328;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 B4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -!-
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CC   ----------------------------------------------------------------------
DR   EMBL; M13788; AAA38506.1; -.
DR   PIR; A02035; MHMSB4.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL     1     19
FT   CHAIN     20    117       IG HEAVY CHAIN V REGION VH558 B4.
FT   DOMAIN    20     49       FRAMEWORK-1.
FT   DOMAIN    50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN    55     68       FRAMEWORK-2.
FT   DOMAIN    69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN    86    117       FRAMEWORK-3.
FT   DISULFID  41    115       BY SIMILARITY.
FT   NON_TER  117    117
SQ   SEQUENCE 117 AA;  12834 MW;  B8862FAC67ABD345 CRC64;

Query Match             52.7%;  Score 393;  DB 1;  Length 117;
Best Local Similarity   65.8%;  Pred. No. 3.6e-31;
 Matches   77;  Conservative   14;  Mismatches   26;  Indels   0;  Gaps   0;

Qy    1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ::| :| || :| || ::|||||||||||||||||||| ::: |||||
Db    1 MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR   117
         :|||||||:||: ||: ||| :|| ||| :||||:||||:||||||||:|:||::
Db   61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCTR   117


RESULT 10
ID   HV10_MOUSE     STANDARD;     PRT;     117 AA.
AC   P01754; P11270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 145 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC   ----------------------------------------------------------------------
DR   EMBL; J00533; AAA38602.1; -.
DR   PIR; C02034; HVMS45.
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DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL     1     19
FT   CHAIN     20    117       IG HEAVY CHAIN V REGION 145.
FT   DOMAIN    20     49       FRAMEWORK-1.
FT   DOMAIN    50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN    55     68       FRAMEWORK-2.
FT   DOMAIN    69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN    86    117       FRAMEWORK-3.
FT   NON_TER  117    117
SQ   SEQUENCE 117 AA;  12921 MW;  D37DE8A3F543E996 CRC64;

Query Match             52.1%;  Score 389;  DB 1;  Length 117;
Best Local Similarity   65.8%;  Pred. No. 8.8e-31;
 Matches   77;  Conservative   15;  Mismatches   25;  Indels   0;  Gaps   0;

Qy    1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ::| :| || :| || ::||||||||||||||||||||| ::: |||||
Db    1 MGWSCIMLFLAATATGVHFQVLQQPGAELVKPGASVKLSSKASGYTFTSYWMHWVKQRP  60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR   117
         :|||||||:||: ||: ||| :|| ||| :||||:||||:||||||||:|:|||
Db   61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCAR   117


RESULT 11
ID   HV04_MOUSE     STANDARD;     PRT;     117 AA.
AC   P01748;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 23 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02030; HVMS23.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL     1     19
FT   CHAIN     20    117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN    20     49       FRAMEWORK-1.
FT   DOMAIN    50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN    55     68       FRAMEWORK-2.
FT   DOMAIN    69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN    86    117       FRAMEWORK-3.
FT   DISULFID  41    115       BY SIMILARITY.
FT   NON_TER  117    117
SQ   SEQUENCE 117 AA;  12772 MW;  C530F829C906F69B CRC64;

Query Match             52.0%;  Score 388;  DB 1;  Length 117;
Best Local Similarity   64.1%;  Pred. No. 1.1e-30;
 Matches   75;  Conservative   15;  Mismatches   27;  Indels   0;  Gaps   0;
```

```
Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||| :::||: ||::|||| | |||||||||||||||| |||: :| |||: ||||
Db    1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAR 117
          |||||| |||| || || || : |||:|| |||||||| ||||||||||||:||||
Db   61 GQGLEWIGNINPNGGGTNYNEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117

RESULT 12
ID   HV52_MOUSE          STANDARD;          PRT;          117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION VH558 A1/A4.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;

Query Match             51.1%;  Score 381; DB 1;  Length 117;
Best Local Similarity   65.5%;  Pred. No. 5.2e-30;
Matches   74;  Conservative  16;  Mismatches  23;  Indels  0;  Gaps  0;

Qy    5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
          |::| || ||::|||||| |||||||||||||||||| |||: :| |||  ||||
Db    5 WIFLFLLSGTAGVHCQVQLQQSGPELVKPGAIVKISCKASGYTFTSYDINWVKQRPGQGL 64

Qy   65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAR 117
          |||| |||| || || || : |||:|| |||||||| |||||||||||:||||
Db   65 EWIGWIYPGDGSTKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117

RESULT 13
ID   HV13_MOUSE          STANDARD;          PRT;          117 AA.
```

```
Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||| :::||: ||::|||| | |||||||||||||||| |||: :| |||: ||||
Db    1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAR 117
          |||||| |||| || || || : |||:|| |||||||| ||||||||||||:||||
Db   61 GQGLEWIGNINPNGGGTNYNEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117

RESULT 12
ID   HV52_MOUSE          STANDARD;          PRT;          117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
CC       modified and this statement is not removed. Usage by and for commercial
CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION VH558 A1/A4.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;

Query Match             51.1%;  Score 381; DB 1;  Length 117;
Best Local Similarity   65.5%;  Pred. No. 5.2e-30;
Matches   74;  Conservative  16;  Mismatches  23;  Indels  0;  Gaps  0;

Qy    5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
          |::| || ||::|||||| |||||||||||||||||| |||: :| |||  ||||
Db    5 WIFLFLLSGTAGVHCQVQLQQSGPELVKPGAIVKISCKASGYTFTSYDINWVKQRPGQGL 64

Qy   65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAR 117
          |||| |||| || || || : |||:|| |||||||| |||||||||||:||||
Db   65 EWIGWIYPGDGSTKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117

RESULT 13
ID   HV13_MOUSE          STANDARD;          PRT;          117 AA.


AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;

Query Match             50.8%;  Score 379; DB 1;  Length 117;
Best Local Similarity   62.0%;  Pred. No. 8.1e-30;
Matches   75;  Conservative  16;  Mismatches  24;  Indels   6;  Gaps   1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          |||||||| |||||||||||||| :|| ||: |:  |:: ||||| ||||:||:  |||
Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   80 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYYGNTGVYAMDYWGQGTSVT 139
          : |:|:||||| ||:::|||| |:| |||||:|| || |:: | |          :|:|
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------WYFDVWGAGTTVT 114

Qy  140 V 140
          |
Db  115 V 115

RESULT 14
ID   HV01_MOUSE          STANDARD;          PRT;          121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
```

```
DR   PIR; A02027; GVMS11.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER    121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;

Query Match            50.8%;   Score 379;  DB 1;  Length 121;
Best Local Similarity  62.0%;   Pred. No. 8.4e-30;
Matches   75;  Conservative  17;  Mismatches  27;  Indels  2;  Gaps  2;

Qy   20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
            | |||||||||| |||:| ||:  .: :| |||:|| |||||| | :| :|:|
Db    1  EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY  60

Qy   80  DPKFQGKATITADTSSNTAYLQLSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139
            :  :|||:|||||:|||||||||| | |||||| | |:|| :|:|
Db   61  NDNLKGKATLTADTSSSTAYIQLSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT  118

Qy  140  V  140
         |
Db  119  V  119

RESULT 15
HV1C_HUMAN
ID   HV1C_HUMAN     STANDARD;     PRT;     147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815556;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02026; EIHUND.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL      1     19
FT   CHAIN      20    147     IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES    20     20     PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID   41    115
FT   CONFLICT   21     21     T -> V (IN REF. 2).
FT   CONFLICT   53     54     IH -> HI (IN REF. 2).
FT   CONFLICT   67     68     VG -> GV (IN REF. 2).
FT   CONFLICT  125    125     MISSING (IN REF. 2).
FT   NON_TER   147    147
SQ   SEQUENCE  147 AA;  16491 MW;  948F9F72A5366C20 CRC64;


Query Match            50.7%;   Score 378.5;  DB 1;  Length 147;
Best Local Similarity  52.6%;   Pred. No. 1.2e-29;
Matches   72;  Conservative  25;  Mismatches  35;  Indels  5;  Gaps  1;

Qy    9  FLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG  68
            ||:| :|||::  ||  ||||||||||||:|:: |||||||||:| ::::| :|||  :|
Db    9  FLVAAATRVHSQTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVG  68

Qy   69  RIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR----EGYYGN  123
            |:| :|:|| :|: |:||||: :|:|||||:||:||:|: |: |:|:||    | |:|
Db   69  WINPNSGGTNYAPRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNF  128

Qy  124  YGVYAMDYWGQGTSVTV  140
         |  :| ||||||| |||
Db  129  DYSYTLDVWGQGTTVTV  145

Search completed: January  6, 2003, 13:15:46
Job time : 8.07071 secs
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                GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:       January  6, 2003, 13:10:51 ; Search time 26.303 Seconds
                                           (without alignments)
                                           1096.702 Million cell updates/sec

Title:        US-09-155-739-4
Perfect score: 746
Sequence:     1 MKCSWVMFFLMAVVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:        671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    SPTREMBL_21:*
              1: sp_archea:*
              2: sp_bacteria:*
              3: sp_fungi:*
              4: sp_human:*
              5: sp_invertebrate:*
              6: sp_mammal:*
              7: sp_mhc:*
              8: sp_organelle:*
              9: sp_phage:*
             10: sp_plant:*
             11: sp_rodent:*
             12: sp_virus:*
             13: sp_vertebrate:*
             14: sp_unclassified:*
             15: sp_rvirus:*
             16: sp_bacteriap:*
             17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
                              SUMMARIES

Result          Query
No.    Score   Match Length DB  ID        Description
-----  -----   ----- ------ --  --        -----------
  1    589     79.0   468   11  Q99L31    Q99L31 mus musculu
  2    494.5   66.3   473   11  Q99L25    Q99L25 mus musculu
  3    480     64.3   109   11  Q9JL85    Q9JL85 mus musculu
  4    478     64.1   473   11  Q9D8L4    Q9D8L4 mus musculu
  5    447.5   60.0   613   11  Q8VCX7    Q8VCX7 mus musculu
  6    443     59.4   146   11  Q92AQ3    Q92AQ3 mus musculu
  7    439     58.8   489   11  Q8VCX4    Q8VCX4 mus musculu
  8    437     58.6   168   11  Q8VDC9    Q8VDC9 mus musculu
  9    431.5   57.8   145   11  Q924R4    Q924R4 mus musculu
 10    431.5   57.8   145   11  Q924R1    Q924R1 mus musculu
 11    429     57.5   481   11  Q91WT1    Q91WT1 mus musculu
 12    425.5   57.2   488   11  Q91WR1    Q91WR1 mus musculu
 13    425.5   57.0   145   11  Q92AQ6    Q92AQ6 mus musculu
 14    425.5   57.0   463   11  Q99LC4    Q99LC4 mus musculu
 15    425     57.0   481   11  Q91WT3    Q91WT3 mus musculu
 16    424     56.8   142   11  Q924Q1    Q924Q1 mus musculu
 17    424     56.8   146   11  Q924R8    Q924r8 mus musculu
 18    424     56.8   474   11  Q8R3H6    Q8R3h6 mus musculu
 19    421.5   56.5   145   11  Q924Q9    Q924q9 mus musculu
 20    421     56.4   140   11  Q924R2    Q924r2 mus musculu
 21    420.5   56.4   145   11  Q924Q7    Q924q7 mus musculu
 22    419.5   56.2   143   11  Q924R0    Q924r0 mus musculu
 23    419.5   56.2   143   11  Q924P9    Q924p9 mus musculu
 24    419.5   56.2   145   11  Q924P7    Q924p7 mus musculu
 25    415     55.6   142   11  Q924Q2    Q924q2 mus musculu
 26    412.5   55.3   278   11  Q921K1    Q921k1 mus musculu
 27    412     55.2   117   11  Q9QXE9    Q9qxe9 mus musculu
 28    408.5   55.2   481   11  Q8VCV5    Q8vcv5 mus musculu
 29    406.5   54.8   143   11  Q924R7    Q924r7 mus musculu
 30    405.5   54.5   145   11  Q924R3    Q924r3 mus musculu
 31    403.5   54.4   159   4   Q96QS0    Q96qs0 homo sapien
 32    401.5   54.1   137   11  Q924R6    Q924r6 mus musculu
 33    401.5   53.8   143   11  Q91VA2    Q91va2 mus musculu
 34    400.5   53.8   141   11  Q924Q4    Q924q4 mus musculu
 35    400.5   53.7   143   11  Q924P6    Q924p6 mus musculu
 36    393.5   53.7   143   11  Q91V67    Q91v67 mus musculu
 37    393     52.7   146   11  Q924Q8    Q924q8 mus musculu
 38    392.5   52.7   143   11  Q924Q5    Q924q5 mus musculu
 39    392     52.6   144   11  Q924P5    Q924p5 mus musculu
 40    390     52.5   140   11  Q924P8    Q924p8 mus musculu
 41    389.5   52.3   139   11  Q924R5    Q924r5 mus musculu
 42    388.5   52.2   118   11  Q921C4    Q921c4 mus musculu
 43    387     52.1   117   11  Q9QXF0    Q9qxf0 mus musculu
 44    383.5   51.9   110   11  Q9JL77    Q9jl77 mus musculu
 45    380     51.4   111   11  Q9D9B8    Q9d9b8 mus musculu
                     50.9
```

ALIGNMENTS

```
RESULT 1
Q99L31
ID   Q99L31;                  PRELIMINARY;      PRT;     468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;

Query Match            79.0%;  Score 589; DB 11;  Length 468;
Best Local Similarity  81.4%;  Pred. No. 7.4e-50;
Matches   114;  Conservative   9; Mismatches   13;  Indels    4;  Gaps    1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||:|||:||||||| |||||||||||||||||||||:||||||||||||:: |||||
Db    1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWKQRP 60
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Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         |||||||  ||| |||| |||| |||| |||||||||||||||||||||||||:||
Db   61 EQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLL 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
        ||  ||   |||||||||||
Db  121 YGGY---YDYWGQGTTITV 136

RESULT 2
Q99L25
ID   Q99L25;        PRELIMINARY;   PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 473 AA; 52449 MW; BE98B9B7986DA155 CRC64;

Query Match             66.3%;  Score 494.5; DB 11;  Length 473;
Best Local Similarity   67.6%;  Pred. No. 1.6e-40;
Matches  96; Conservative  19; Mismatches 24; Indels  3; Gaps  2;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         |||  : :|||||:| |:||||||||||||||||||:||: |||: | |||||
Db    1 MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREG- 119
         |||||||||||||||||||||||||:|||||||||||||||||||||||| ||: | |
Db   61 EQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS 120

Qy  120 -YYGNYGVYAMDYWGQGTSVTV 140
         ||| |||||   |||||||:||
Db  121 IYYG-YGLYYFDYWGQGTTITV 141

RESULT 3
Q9JL85
ID   Q9JL85;        PRELIMINARY;   PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2001 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
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RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206021; AAF69319.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      109    109
SQ   SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match             64.3%;  Score 480; DB 11;  Length 109;
Best Local Similarity   80.5%;  Pred. No. 7.1e-40;
Matches 91; Conservative  8; Mismatches  8; Indels  6; Gaps  1;

Qy   28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
         ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db    1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy   88 TITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
         ||:||||||||||||||||||||||||||||:     ||:|||||||||:|||
Db   61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR-----GAVVFDYWGQGTALTV 107

RESULT 4
Q9D8L4
ID   Q9D8L4;        PRELIMINARY;   PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009Rik protein.
GN   IGH-1 OR 1810060009RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK079918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
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RESULT 6
Q924Q3
ID   Q924Q3      PRELIMINARY;      PRT;   146 AA.
AC   Q924Q3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067797; BAB63282.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1      1
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;   16136 MW;  CEA8DD6E1955807F CRC64;

Query Match             59.4%;  Score 443;  DB 11;  Length 146;
Best Local Similarity   71.1%;  Pred. No. 4.6e-36;
  Matches   86;  Conservative  14;  Mismatches  19;  Indels   2;  Gaps   1;

Qy       20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
            :|||| ||||||||||||||||||:||||||| ||||||||  :|:|||||  :|:|||
Db        1 QVQLQQPGAELVKPGASVKLSCKASGYTFSYWMHWVKQPRGRGLEWIGRIDPNSGGTKY  60

Qy       80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
            : ||: ||: |:||| ||||||||||||||||:|||  ::|| ||||||||||||||||
Db       61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSLY--DYGDYAMDYWGQGTSVT 118

Qy      140 V 140
            | |
Db      119 V 119
```

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RESULT 7
Q8VCX4
ID   Q8VCX4      PRELIMINARY;      PRT;   489 AA.
AC   Q8VCX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 53.2 kDa protein.
GN   AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018322; AAH18322.1; -.
DR   MGD; MGI:2144917; AI893585.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Left column:

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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;   51699 MW;  9DED57A514475FBB CRC64;

Query Match             64.1%;  Score 478;  DB 11;  Length 473;
Best Local Similarity   67.1%;  Pred. No. 6.8e-39;
  Matches   94;  Conservative  19;  Mismatches  23;  Indels   4;  Gaps   2;

Qy        1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
            |:||| ||::| ||:|| ||  ||||||||||||||||||||||||||| ||||||||||
Db        1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKLPKGASVKICKASGYTFSYWIEWVKQRP  60

Qy       61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            |||||||||||| : |:||| : : |||:||||||||||||||||||||||:||||||| ||
Db       61 GQGLEWIGRIDPDNGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDSAVYFCARSGY 120

Qy      121 YGNYGVYAMDYWGQGTSVTV 140
             :| :| |||||| ||||| |||
Db      121 --DYDWFA--YWGQGTLVTV 136
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RESULT 5
Q8VCX7
ID   Q8VCX7      PRELIMINARY;      PRT;   613 AA.
AC   Q8VCX7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 67.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018315; AAH18315.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;   67855 MW;  41A9384DD4C22862 CRC64;

Query Match             60.0%;  Score 447.5;  DB 11;  Length 613;
Best Local Similarity   62.1%;  Pred. No. 9.7e-36;
  Matches   87;  Conservative  19;  Mismatches  29;  Indels   5;  Gaps   1;

Qy        1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
            | :|| ||::| ||:|| ||  ||||||||||||||| :||:|| :| |||||||
Db        1 MEWTWVFLFLLSVTAGVHSQVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRP  60

Qy       61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            |||||||||| |:|:|||||| :||: ||:||||||||||||||||||||:|||||||
Db       61 GHGLEWIGEILPGSGSTNYNEKFKGKATTTADTSSNTAYMQLSSLTSEDSAVYYCAR--- 117

Qy      121 YGNYGVYAMDYWGQGTSVTV 140
             :| : || |||| |||| |
Db      118 --RLGRWYFDVWGAGTTVTV 135
```

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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;   51699 MW;  9DED57A514475FBB CRC64;
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KW   Hypothetical protein.
SQ   SEQUENCE   489 AA;   53208 MW;  CC85B1194DAFEF2C CRC64;

Query Match             58.8%;  Score 439; DB 11;  Length 489;
Best Local Similarity   62.7%;  Pred. No. 5.1e-35;
  Matches  89;  Conservative  16;  Mismatches  35;  Indels   2;  Gaps   2;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |: || ||| | |||| |||||||||||||||||||||||||||| |||: :|| :||
Db      1 MEWCWVFLFLLSVTAGVHSKVQLQQSGAELVKPGASVKLSCKASGYTFSDYFIHWIKQRS 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||| |: :| :|| ||:||| |  |: ||||||||||||||||||||||||||||
Db     61 GQGLEWIGWFNPGSGSIKFNEKPKDKATLTADKSSTTVYMDLSRLTSEDSAVYFCARHED 120

Qy    121 YGNY-GVYA-MDYWGQGTSVTV 140
          ||| |  |  |||||||||
Db    121 RGNYDGSLAWFVYWGQGTLVTV 142


RESULT 8
ID   Q8VDC9     PRELIMINARY;   PRT;   168 AA.
AC   Q8VDC9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Anti-MOG z12 variable gamma 2a (Fragment).
GN   IGG2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Chernajovsky Y.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Sembi P.;
RT   "Targeting T cells to the CNS.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416332; CAC94867.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR001230; Prenyl_site.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
FT   NON_TER   168    168
SQ   SEQUENCE   168 AA;   18293 MW;  1E3719FCC0E72723 CRC64;

Query Match             58.6%;  Score 437; DB 11;  Length 168;
Best Local Similarity   60.6%;  Pred. No. 2.1e-35;
  Matches  86;  Conservative  19;  Mismatches  29;  Indels   8;  Gaps   2;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |: :|| ||||||:||:|:|||||||||||||||||||||||| :| :||: ||||
Db      1 MEWTWVFLFLLSVTAGVHSQVQLQQSGAELMKPGASVKISCKATGYTFSSYWIDWVKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||| |: ||  :|||| ||| :|| |: ||||||||||||||||||||:||||
Db     61 GHGLEWIGEILPGSGRTNYNEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYYCA---- 116

Qy    121 YGNYGV--YAMDYWGQGTSVTV 140
          |||||   :|||||||||||
Db    117 --NYGSSRWYFDVWGAGTTVTV 136
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RESULT 9
Q924R4
ID   Q924R4     PRELIMINARY;   PRT;   145 AA.
AC   Q924R4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067785; BAB63270.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1     1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA;   16081 MW;  ECDB1A135E05B8AA CRC64;

Query Match             57.8%;  Score 431.5; DB 11;  Length 145;
Best Local Similarity   70.2%;  Pred. No. 6.2e-35;
  Matches  85;  Conservative  14;  Mismatches  19;  Indels   3;  Gaps   2;

Qy     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          :|||||||||||||||||||||||||||||||||||| ||: :|||||||||||||||||
Db      1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNTGVYAMDYWGQGTSVT 139
          : || :||| |||||:||||||||||||||:||||:||| : -|||||||||||||||||
Db     61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDY--DYD-YAMDYWGQGTSVT 117

Qy    140 V 140
          |
Db    118 V 118


RESULT 10
Q924R1
ID   Q924R1     PRELIMINARY;   PRT;   145 AA.
AC   Q924R1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067789; BAB63274.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1     1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA;   15979 MW;  0162D0A26C746C04 CRC64;

Query Match             57.8%;  Score 431.5; DB 11;  Length 145;
Best Local Similarity   69.4%;  Pred. No. 6.2e-35;
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Matches    84;   Conservative   13;   Mismatches   21;   Indels    3;   Gaps    1;

Qy    20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
          :||||  ||||||||||||||||| ||:    ::| |||||  :||||||||| :| |||
Db     1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  60

Qy    80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139
          : ||: |:|||:| |:|||:||||||||||||||:|||   ---YDGSSFYAMDYWGQGTSVT  117
Db    61  NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR---YDGSSFYAMDYWGQGTSVT  117

Qy   140  V 140
          :| |||||||:|
Db   118  V 118
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RESULT 11
Q91WT1
ID   Q91WT1   PRELIMINARY;   PRT;   481 AA.
AC   Q91WT1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 52.1 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013490; AAH13490.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA;   52105 MW;   97DF68D159463F65 CRC64;

```
Query Match     57.5%;   Score 429;   DB 11;   Length 481;
Best Local Similarity   61.8%;   Pred. No. 4.8e-34;
Matches    84;   Conservative   16;   Mismatches   30;   Indels    6;   Gaps    1;

Qy     5  WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL  64
          |:  |: | ||| ||  |:|||||||||||||||||||| ||:  ::| ||||| :||:|
Db     5  WIFLFLLSGTAGVQCQVQLLQSGPELVKPGASVKISCKASGYTFTSYIHWVKQRPGQGL  64

Qy    65  EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNY  124
          |||||||| : || ||:|:|:|||:|:|||:||||||||||| |
Db    65  VWIGWIYPGDGNTKYNEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFCTRG------  118

Qy   125  GVYAMDYWGQGTSVTV  140
          : :| ||||||||:||
Db   119  GGWAFDYWGQGTLTV  134
```

RESULT 12
Q91WR1
ID   Q91WR1   PRELIMINARY;   PRT;   488 AA.
AC   Q91WR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 53.0 kDa protein.
GN   AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;

RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013539; AAH13539.1; -.
DR   MGD; MGI:2144917; AI893585.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   488 AA;   52964 MW;   F12068460B400B9D CRC64;

```
Query Match     57.2%;   Score 426.5;   DB 11;   Length 488;
Best Local Similarity   59.6%;   Pred. No. 8.6e-34;
Matches    84;   Conservative   21;   Mismatches   35;   Indels    1;   Gaps    1;

Qy     1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
          : :|: ||| | :|||||||||||||||||||||||||||||||||||||||
Db     1  MGWNWIFLFLLSGTAGIYSEVQLQQSGPELVKPGASVKLSCKASGYTITDYVNWVKQSH  60

Qy    61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY  120
          :|||| |:|||||:|:||:|: ||||:|:|| ||:|::|:||::|:|||:||::|||:|||
Db    61  GKSLEWIGDINPYNGGTSYNQKFKGKATLIVDKSSSIAYMQLNNLTSDDSAVYYCARGPV  120

Qy   121  YGNYGVYAM-DYWGQGTSVTV  140
          ||||   || ||||||||:||
Db   121  YYSYFSYDRGDYWGQGTLVTV  141
```

RESULT 13
Q92406
ID   Q92406   PRELIMINARY;   PRT;   145 AA.
AC   Q92406;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067794; BAB63279.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA;   16011 MW;   9BC0846D40DF97EA CRC64;

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Query Match     57.0%;   Score 425.5;   DB 11;   Length 145;
Best Local Similarity   68.3%;   Pred. No. 2.4e-34;
Matches    84;   Conservative   14;   Mismatches   18;   Indels    7;   Gaps    2;

Qy    20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
          :|||| ||||||||||||||||||||:|||||||||||||||  ::| ||||||:  |||
Db     1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  60

Qy    80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE--GYYGNYGVYAMDYWGQGTS  137
          :||:|:|||:| |:|||:|||||||||||||||:||| |  ||:|||:|||||||||||
Db    61  NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSTLSHY----YAMDYWGQGTS  115

Qy   138  VTV 140
          ||| |
Db   116  VTV 118
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RESULT 14
Q99LC4
ID   Q99LC4   PRELIMINARY;   PRT;   463 AA.

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AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC03435; AAH03435.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   463 AA;   51007 MW;  EAA674C6BBC30783 CRC64;

Query Match             57.0%;  Score 425.5;  DB 11;  Length 463;
Best Local Similarity   59.3%;  Pred. No. 1e-33;
Matches    83;  Conservative   21;  Mismatches   33;  Indels    3;  Gaps    2;

Qy          1 MKCSWVMFFLMAVVTGVNSEVOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              | : |  : | | :| |||||||:||||||||: ||| :||||||| : ||
Db          1 MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRT 60

Qy         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              ||||||| : :  :| | | : | |||||||: |: ||::: |||||||:|:|||||  |
Db         61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120

Qy        121 YGNYGVYAMDYWGQGTSVTV 140
              | ::|::|  ||||||: |||
Db        121 Y-SYDLFA--YWGQGTLVTV 137
```

```
-SQ. SEQUENCE   481 AA;   52022 MW;  4EEB5C253038B718 CRC64;

Query Match             57.0%;   Score 425;  DB 11;  Length 481;
Best Local Similarity   58.6%;   Pred. No. 1.2e-33;
Matches    85;  Conservative   21;  Mismatches   23;  Indels   16;  Gaps    3;

Qy          1 MKCSWVMFFLMAVVTGVNSEVOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
              |:| : : ||: |||||||:|| ||||:|: ||||||| ||: :|:: ||||
Db          1 MRWSCIILFLVATATGVNSQVQLQQPGAEIVRPGASVKLSCKTSGYTFTDYWMNWVKQRP 60

Qy         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR--- 117
              ||||||| | | | :|  | : |:::||||||:::: | ||||||: :|||||||||
Db         61 GQGLEWIGAIDPFDSYTSYNQKFKG-TLTVDTSSSSAYMLLSSLTSEDSAVYFCARGPR 119

Qy        118 --EGYGNYGVYAMDYWGQGTSVTV 140
                || | :
Db        120 DSSGY-------YWGQGTTLTV 134

Search completed: January  6, 2003, 13:17:27
Job time : 27.303  secs
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RESULT 15
Q91WT3
ID   Q91WT3        PRELIMINARY;      PRT;    481 AA.
AC   Q91WT3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
GN   AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013488; AAH13488.1; -.
DR   MGD; MGI:2144917; AI893585.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein; Immunoglobulin domain.
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```
            GenCore version 5.1.3
    Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    January  6, 2003, 12:46:55 ; Search time 24.6263 Seconds
                                          (without alignments)
                                          573.557 Million cell updates/sec

Title:           US-09-155-739-7
Perfect score:   562
Sequence:        1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:        908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_101002:*
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              3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
              4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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              9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
             10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	562	100.0	106	16	AAR81321	Humanized anti-VLA
2	562	100.0	106	18	AAW22412	Humanised alpha-4
3	562	100.0	126	18	AAW22419	Humanised alpha-4
4	508	90.4	106	16	AAR81328	Mouse anti-VLA-4 a
5	508	90.4	126	16	AAR81326	Mouse VLA-4 antibo
6	508	90.4	126	16	AAR81332	Human VLA-4 reshap
7	508	90.4	126	18	AAW22409	Alpha-4 integrin m
8	488	86.8	359	20	AAY29913	Human MCP-3 and mu
9	488	86.8	361	20	AAY29911	Human IP-10 and mu
10	488	86.8	374	20	AAY29916	Artificial synthet
11	481	85.6	128	15	AAR60627	ME1-14 light chain
12	475.5	84.6	234	12	AAR13050	CD4-specific CDR-g
13	471.5	83.9	107	16	AAR78970	Light chain variab
14	465	82.7	108	17	AAR93159	Murine monoclonal
15	460.5	81.9	128	11	AAR06252	Variable region of
16	460	81.9	637	13	AAR26983	(FRP51)-ETA fusion
17	456	81.1	109	19	AAW26797	Anti-gp54 MAb T16
18	455	81.0	240	16	AAR85495	ScFv(FWP51). Synt
19	455	81.0	241	20	AAY21882	Amino acid sequenc
20	455	81.0	245	19	AAW26800	Anti-gp54 MAb T16
21	453.5	80.7	107	16	AAR81322	Humanized VLA-4 an
22	453.5	80.7	107	18	AAW22422	Humanised alpha-4
23	453	80.6	109	12	AAR13658	Murine OKT4A light
24	452	80.4	241	13	AAR26981	FWP51 fusion prote
25	451.5	80.3	108	16	AAR65163	Human REI monoclon
26	451.5	80.3	129	15	AAR47207	Human/murine IL-1
27	451	80.2	355	18	AAW35133	R. pipiens recombi
28	449.5	80.0	107	19	AAW86805	Variable Light dom
29	449.5	80.0	107	19	AAW70625	Humanised murine a
30	449.5	80.0	107	23	ABP61194	Humanised anti-VEG
31	446.5	79.4	108	18	AAW10231	CDR-grafted light
32	446.5	79.4	110	19	AAW70673	Anti-VEGF humanise
33	446.5	79.4	110	23	ABP61242	Humanised anti-VEG
34	446.5	79.4	234	18	AAW10233	TF8-5G9 CDR-grafte
35	446.5	79.4	237	19	AAW70703	Protein encoded by
36	446.5	79.4	650	23	ABP61241	Phage-display anti
37	445.5	79.3	107	19	AAW86804	Variable Light dom
38	445.5	79.3	107	19	AAW70623	Humanised murine a
39	445.5	79.3	107	23	ABP61192	Humanised anti-VEG
40	444.5	79.1	107	20	AAW87455	Humanised anti-alp
41	444.5	79.1	107	22	AAB62087	Human V1 consensus
42	444.5	79.1	107	22	AAB60400	Consensus human li
43	444.5	79.1	107	22	AAB61585	Human variable lig
44	444.5	79.1	108	19	AAW70622	Human consensus fr
45	444.5	79.1	108	21	AAY82345	Human consensus se

ALIGNMENTS

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RESULT 1
AAR81321
ID   AAR81321 standard; Protein; 106 AA.
XX
AC   AAR81321;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Chimeric Mus musculus.
OS   Chimeric Homo sapiens.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
```

XX
PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanized antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (See
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence 106 AA;

Query Match   100.0%; Score 562; DB 16; Length 106;
Best Local Similarity   100.0%; Pred. No. 1.2e-36;
Matches 106; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106

RESULT 2
AAW22412
ID   AAW22412 standard; Protein; 106 AA.
XX
AC   AAW22412;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key   Location/Qualifiers
FT   Region   1..23
FT   /label= FR1
FT   /note= "REI framework region 1"
FT   Region   24..34
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   35..49
FT   /label= FR2
FT   /note= "REI framework region 2"
FT   Misc-difference 45
FT   /note= "REI Lys-45 is substd. by Lys of mouse
FT   21.6 VL, important in supporting the
FT   CDR2 loop"
FT   Misc-difference 49

FT   /note= "REI Tyr-49 is substd. by His of mouse
FT   21.6 VL, located at the binding site"
FT   Region   50..56
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   57..88
FT   /label= FR3
FT   /note= "REI framework region 3"
FT   Misc-difference 58
FT   /note= "REI Val-58 is substd. by Ile of mouse
FT   21.6 VL, important in supporting the CDR2
FT   loop"
FT   Misc-difference 69
FT   /note= "REI Thr-69 is substd. by Arg of mouse
FT   21.6 VL, involved in antibody-antigen
FT   binding"
FT   Region   89..96
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
FT   Region   97..106
FT   /label= FR4
FT   /note= "REI framework region 4"
FT   Misc-difference 103
FT   /note= "REI Leu-103 substd. by Val, more typical
FT   of human kappa light chain J region"
FT   Misc-difference 104
FT   /note= "REI Gln-104 substd. by Glu, more typical
FT   of human kappa light chain J region"
FT   Misc-difference 106
FT   /note= "REI Thr-106 substd. by Lys, more typical
FT   of human kappa light chain J region"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 6; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha 4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence 106 AA;

```
Query Match           100.0%;  Score 562; DB 18;  Length 106;
Best Local Similarity 100.0%;  Pred. No. 1.2e-36;
Matches 106;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106

RESULT 3
AAW22419
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..20
FT                  /label= Leader
FT   Protein        21..126
FT                  /label= Mat_protein
FT                  /note= "VL version La (Claim 25)"
FT   Region         21..43
FT                  /label= FR1
FT                  /note= "REI framework region 1"
FT   Region         44..54
FT                  /label= CDR1
FT                  /note= "21.6 complementarity determining region 1"
FT   Region         55..69
FT                  /label= FR2
FT                  /note= "REI framework region 2"
FT   Region         70..76
FT                  /label= CDR2
FT                  /note= "21.6 complementarity determining region 2"
FT   Region         77..108
FT                  /label= FR3
FT                  /note= "REI framework region 3"
FT   Region         109..116
FT                  /label= CDR3
FT                  /note= "21.6 complementarity determining region 3"
FT   Region         117..126
FT                  /label= FR4
FT                  /note= "REI framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
```

```
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412). It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;

Query Match           100.0%;  Score 562; DB 18;  Length 126;
Best Local Similarity 100.0%;  Pred. No. 1.4e-36;
Matches 106;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  81 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 126

RESULT 4
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996 (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Region         1..23
FT                  /label= FR1
FT                  /note= "mouse light chain variable framework
FT                  region 1"
FT   Region         24..34
FT                  /label= CDR1
FT                  /note= "mouse light chain variable complementarity
FT                  determining region 1"
FT   Region         35..49
FT                  /label= FR2
FT                  /note= "mouse light chain variable framework
FT                  region 2"
FT   Region         50..56
FT                  /label= CDR2
FT                  /note= "mouse light chain variable complementarity
FT                  determining region 2"
```

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FT   Region             57..88
FT                      /label= FR3
FT                      /note= "mouse light chain variable framework
FT                      region 3"
FT   Region             89..96
FT                      /label= CDR3
FT                      /note= "mouse light chain variable complementarity
FT                      determining region 3"
FT   Region             97..106
FT                      /label= FR4
FT                      /note= "mouse light chain variable framework
FT                      region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure: Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;

Query Match             90.4%;  Score 508;  DB 16;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 1.8e-32;
Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||| :|||||||||||||||| || |||||||||||||||||||||||
Db      1 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||| ||:|:|||||||||||||||||||||||||:|||
Db     61 RFSGSGSGRDYSFNISNLEPEDIATYCLQYDNLWTFGGGTKLEIK 106
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RESULT 5
AAR81326
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ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;

Query Match             90.4%;  Score 508;  DB 16;  Length 126;
Best Local Similarity   88.7%;  Pred. No. 2.2e-32;
Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy      1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS   60
           |||||||||||| | :|||||||||||||| ||| ||||||||||||||||||||
Db     21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHPGKRPRLLIHYTSALQPGIPS    80

Qy     61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK               106
           |||||||||:| ||||:| :|||||||||||||||||| ||:|||
Db     81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK               126

RESULT 6
AAR81332
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions. In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis. They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis. The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence 126 AA;

Query Match             90.4%;  Score 508;  DB 16;  Length 126;
Best Local Similarity   88.7%;
Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS   60
           |||||||||||| | :|||||||||||||| ||| ||||||||||||||||||||
Db      1  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHPGKRPRLLIHYTSALQPGIPS    60

Qy     61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK               106
           |||||||||:| ||||:| :|||||||||||||||||| ||:|||
Db     61  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK               106

RESULT 7
AAW22409
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
```

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XX
PR  21-NOV-1995;  95US-0561521.
XX
PA  (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI  Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR  WPI; 1997-297879/27.
DR  N-PSDB; AAT74759.
XX
PT  Uses of humanised alpha-4 integrin antibody - for treatment of
PT  asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS  Claim 18; Page 68; 107pp; English.
XX
CC  This polypeptide comprises the light chain variable region (VL) of
CC  mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC  complementarity determining regions (CDRs) of the 21.6 VL can be
CC  incorporated into a human REI framework to produce a claimed
CC  humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC  antibody that is used in the manufacture of a medicament for
CC  treating a disease selected from asthma, atherosclerosis, AIDS,
CC  dementia, diabetes, inflammatory bowel disease, rheumatoid
CC  arthritis, transplant rejection, graft versus host disease, tumour
CC  metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC  ischaemia, and acute leukocyte mediated lung injury. The antibody
CC  may also be used in the affinity purification of alpha-4 integrin
CC  for use as a vaccine or an immunogen. It is also useful for
CC  generating idiotypic antibodies. The humanised antibodies of the
CC  invention have a half-life in the human circulation essentially
CC  equivalent to that of naturally occurring human antibodies.
XX
SQ  Sequence  126 AA;

Query Match        90.4%;    Score 508; DB 18;  Length 126;
Best Local Similarity  88.7%;    Pred. No. 2.2e-32;
Matches   94;  Conservative   6;  Mismatches   6;  Indels   0;  Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||||||:|||||||||||||||||||||| ||||||||||||||||||||
Db  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQQTPGKRPRLLIHYTSALQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKVEIK 106
       |||||||||||:||:|||||||||||||||||||||||||||:||:|
Db  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126

RESULT 8
AAY29913
ID  AAY29913 standard; Protein; 359 AA.
XX
AC  AAY29913;
XX
DT  17-NOV-1999  (first entry)
XX
DE  Human MCP-3 and murine scFv38 fusion protein.
XX
KW  Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW  immune response; HIV; infection.
XX
OS  Homo sapiens.
OS  Mus sp.
OS  Synthetic.
XX
PN  WO9946392-A1.
XX
PD  16-SEP-1999.
XX
PF  12-MAR-1999;  99WO-US05345.
XX
PR  12-MAR-1998;  98US-0077745.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Kwak LW, Biragyn A;
XX
DR  WPI; 1999-551418/46.
XX
PT  New fusion polypeptides comprising a chemokine and a tumour antigen or
PT  HIV antigen, used for treating cancers or treating or preventing HIV
PT  infection -
XX
PS  Disclosure; Page 118-119; 142pp; English.
XX
CC  The present invention describes fusion proteins comprising a chemokine
CC  and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC  comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC  Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC  (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC  SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC  HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC  gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC  be used for producing an immune response, e.g. an effector T cell immune
CC  response. They can also be used for treating cancer or treating or
CC  preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC  can be used in in vitro diagnostic assays, as well as in screening assays
CC  for identifying unknown tumour antigen epitopes and fine mapping of
CC  tumour antigen epitopes. The present sequence represents a fusion protein
CC  from the present invention.
XX
SQ  Sequence  359 AA;

Query Match        86.8%;    Score 488;  DB 20;  Length 359;
Best Local Similarity  84.9%;    Pred. No. 2e-30;
Matches   90;  Conservative   9;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  233 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 292

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKVEIK 106
        |||||||||||:||:||||||||||||||||:|||||||||||||:|
Db  293 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 338

RESULT 9
AAY29911
ID  AAY29911 standard; Protein; 361 AA.
XX
AC  AAY29911;
XX
DT  17-NOV-1999  (first entry)
XX
DE  Human IP-10 and murine scFv38 fusion protein.
XX
KW  Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW  immune response; HIV; infection.
XX
OS  Homo sapiens.
OS  Mus sp.
OS  Synthetic.
XX
PN  WO9946392-A1.
XX
PD  16-SEP-1999.
XX
PF  12-MAR-1999;  99WO-US05345.
XX
PR  12-MAR-1998;  98US-0077745.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Kwak LW, Biragyn A;
XX
DR  WPI; 1999-551418/46.
XX
```

PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 115-116; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC   comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC   Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC   (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC   SDF-1 and HIV gp120; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC   HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC   gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC   be used for producing an immune response, e.g. an effector T cell immune
CC   response. They can also be used for treating cancer or treating or
CC   preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC   can be used in in vitro diagnostic assays, as well as in screening assays
CC   for identifying unknown tumour antigen epitopes and fine mapping of
CC   tumour antigen epitopes. The present sequence represents a fusion protein
CC   from the present invention.
XX
SQ   Sequence   361 AA;
XX
      Query Match   86.8%;   Score 488; DB 20; Length 361;
      Best Local Similarity 84.9%; Pred. No. 2e-30;
      Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 294

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGQTKVEIK 106
             ||||||||||:||:|:||||||||||||||||||||| ||| ||||
Db   295 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 340

RESULT 10
AAY29916
ID   AAY29916 standard; Protein; 374 AA.
XX
AC   AAY29916;
XX
DT   17-NOV-1999 (first entry)
XX
DE   Artificial synthetic construct protein SEQ ID NO:15.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05345.
XX
PR   12-MAR-1998; 98US-0077745.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 117-118; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine

CC   and a tumour antigen or HIV antigen. Specifically claimed fusion
CC   proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC   human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC   Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC   human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC   MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC   HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC   can be used for producing an immune response, e.g. an effector T cell
CC   immune response. They can also be used for treating cancer or treating
CC   or preventing HIV infection. The fusion proteins and/or nucleotide
CC   sequences can be used in in vitro diagnostic assays, as well as in
CC   screening assays for identifying unknown tumour antigen epitopes and fine
CC   mapping of tumour antigen epitopes. AAY29916 and AA221168 are
CC   sequences given in the SEQ ID LISTING in the present invention but which
CC   are not mentioned further within the specification.
XX
SQ   Sequence   374 AA;
XX
      Query Match   86.8%;   Score 488; DB 20; Length 374;
      Best Local Similarity 84.9%; Pred. No. 2.1e-30;
      Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 154

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGQTKVEIK 106
             ||||||||||:||:|:||||||||||||||||||||| ||| ||||
Db   155 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200

RESULT 11
AAR60627
ID   AAR60627 standard; Protein; 128 AA.
XX
AC   AAR60627;
XX
DT   04-JUN-1995 (first entry)
XX
DE   ME1-14 light chain variable region.
XX
KW   Monoclonal antibody; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9421294-A.
XX
PD   29-SEP-1994.
XX
PF   14-MAR-1994; 94WO-US02724.
XX
PR   19-MAR-1993; 93US-0033864.
XX
PA   (BIGN/) BIGNER D D.
PA   (CARR/) CARREL S.
PA   (ZALU/) ZALUTSKY M R.
XX
PI   Bigner DD, Carrel S, Zalutsky MR;
XX
DR   WPI; 1994-316669/39.
DR   N-PSDB; AAQ73537.
XX
PT   Method of treating solid or cystic tumours with antibodies - by
PT   administering monoclonal antibody Mel-14, having Fc deleted,
PT   using injection or deposition in the cyst cavity
XX
PS   Disclosure; Fig 2; 31pp; English.
XX
CC   The sequence is that of the ME1-14 light chain. The protein is a
CC   monoclonal antibody which can be administered to treat solid or
CC   cystic tumours.
CC   See also AAR60626.
XX

```
SQ  Sequence  128 AA;

Query Match      85.6%;   Score 481;  DB 15;  Length 128;
Best Local Similarity  84.0%;   Pred. No. 2.7e-30;
Matches  89;   Conservative  9;  Mismatches  8;  Indels  0;  Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||: :|||||| |||||:|||||| ||| ||||||:||||| |||||||
Db  21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||||:||||||||||||||||||:|||||| |||||:|||
Db  81 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGGTKLEIK 126

RESULT 12
AAR13050
ID  AAR13050 standard; Protein; 234 AA.
XX
AC  AAR13050;
XX
DT  27-SEP-1991  (first entry)
XX
DE  CD4-specific CDR-grafted light chain.
XX
KW  variable region; antibody; OKT4A; heavy chain; CD4;
KW  complementary determining region.
XX
OS  Synthetic.
XX
FH  Key         Location/Qualifiers
FT  Peptide     1..20
FT              /label= signal sequence
FT  Region      21..45
FT              /label= framework region 1
FT  Region      46..52
FT              /label= CDR 1
FT  Region      53..69
FT              /label= framework region 2
FT  Region      70..76
FT              /label= CDR 2
FT  Region      77..110
FT              /label= framework region 3
FT  Region      111..116
FT              /label= CDR 3
FT  Region      117..132
FT              /label= framework region 4
FT  Region      133..234
FT              /label= kappa constant domain
XX
PN  WO9109966-A.
XX
PD  11-JUL-1991.
XX
PF  21-DEC-1990;   90WO-GB02015.
XX
PR  21-DEC-1989;   89GB-0028874.
PR  90WO-GB02017.
PR  21-DEC-1990;   90WO-GB02018.
XX
PA  (ORTH ) ORTHO PHARM CORP.
XX
PI  Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
XX
DR  WPI; 1991-222914/30.
DR  N-PSDB; AAQ12633.
XX
PT  New CD4 specific recombinant - complementarity determining region
PT  grafted antibody for treating graft rejection and T cell
PT  disorders
XX
PS  Claim 1; Fig 8; 96pp; English.
XX


CC  This is an example of a CDR-grafted light chain of the invention.
CC  The constant regions are based on sequences of the human kappa
CC  constant domain, the signal sequence is derived from murine MAb
CC  B72.3 and the CDR sequences are based on the murine OKT4A light chain
CC  CDRs. The recombinant antibody encoded by this sequence has affinity
CC  for CD4 similar to that of OKT4A.
CC  See also AAQ12627-Q12632.
XX
SQ  Sequence  234 AA;

Query Match      84.6%;   Score 475.5;  DB 12;  Length 234;
Best Local Similarity  84.9%;   Pred. No. 1.3e-29;
Matches  90;   Conservative  8;  Mismatches  7;  Indels  1;  Gaps  1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||||||||||||||||||||||||:|||||||:||:|:|:|
Db  21 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYTSTLQPGVPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
        ||||||| :|||||||||||||||||| ||| :||||||||||:|
Db  81 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDNLLFTFGGGTKLQI 126

RESULT 13
AAR78970
ID  AAR78970 standard; Protein; 107 AA.
XX
AC  AAR78970;
XX
DT  21-DEC-1995  (first entry)
XX
DE  Light chain variable region for monoclonal antibody 23F8.
XX
KW  Monoclonal antibody; heavy metal; mercury; variable region;
KW  light chain.
XX
OS  Synthetic.
XX
PN  WO9520607-A.
XX
PD  03-AUG-1995.
XX
PF  27-JAN-1995;   95WO-US01199.
XX
PR  27-JAN-1994;   94US-0187407.
XX
PA  (BION-) BIONEBRASKA INC.
XX
PI  Lopez O, Wagner FW, Wylie DE;
XX
DR  WPI; 1995-275415/36.
DR  N-PSDB; AAQ97508.
XX
PT  New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT  monoclonal antibodies, used for detecting, removing, adding or
PT  neutralising heavy metals
XX
PS  Claim 23; Page 67-68; 106pp; English.
XX
CC  Hybridoma antibodies have been produced with the spleen cells of
CC  BALB/c mouse that had received multiple injections of mercuric ions
CC  reacted with glutathione to produce a mercuric ion coordinate
CC  covalent compound which was covalently bound to keyhole limpet
CC  hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC  5B6 and 3E8) were producing MAbs that were strongly positive
CC  against glutathione-mercuric ions but negative against glutathione
CC  without mercuric ions. RNA was isolated from hybridoma cells with
CC  guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC  by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC  were complementary to the 5' end of the CH1 domain of the heavy
CC  chain expressed by the hybridoma of interest, or to the 5' and of
CC  the C kappa domain. Some of the primers used for cDNA synthesis are
CC  shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
```

```
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate v-region primer. In addition, the VH primer AAQ97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC   AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
XX
SQ   Sequence  107 AA;

Query Match             83.9%;  Score 471.5;  DB 16;  Length 107;
Best Local Similarity   83.2%;  Pred. No. 1.3e-29;
Matches   89;  Conservative   9;  Mismatches   8;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||:| :|||||| |||||||| ||| || |||||||| |||||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHPKGKGPRLLIHYTSIQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
         |||||||||||:|:||||:||||||||||||| :|||||||||:|||
Db   61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107

RESULT 14
AAR93159
ID   AAR93159 standard; Protein; 108 AA.
XX
AC   AAR93159;
XX
DT   24-OCT-1996 (first entry)
XX
DE   Murine monoclonal antibody K20 kappa chain variable region.
XX
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementarity determining region; CDR.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "framework region"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "complementarity determining region"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "framework region"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "complementarity determining region"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "framework region"
FT   Region          89..94
FT                   /label= CDR3
FT                   /note= "complementarity determining region"
FT   Region          95..108
FT                   /label= J_kappa1
XX
PN   FR2724393-A1.
XX
PD   15-MAR-1996.
XX
PF   12-SEP-1994;  94FR-0010858.
XX
PR   12-SEP-1994;  94FR-0010858.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA   (PROT-) PROTEINE PERFORMANCE SA.
XX
PI   Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI   Poul MA;
XX
DR   WPI; 1996-162083/17.
DR   N-PSDB; AAT26849.
XX
PT   Humanisation of non-human immunoglobulin variable regions - for
PT   prodn. of humanised antibodies, esp. K20, e.g. as an
PT   immunosuppressant
XX
PS   Example 1; Fig 2A; 39pp; French.
XX
CC   The present sequence is that of the variable region of the kappa
CC   light chain from murine monoclonal antibody K20. The antibody
CC   recognises the beta 1 subunit (CD29) of integrins and inhibits
CC   activation and proliferation of peripheral T cells induced by
CC   anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC   for humanisation; the humanised version may be useful as an
CC   immunosuppressant. In the humanisation process, the complementarity
CC   determining regions (CDRs) of a human antibody with framework
CC   regions 70-95% homologous to those of K20 were replaced by the K20
CC   CDRs.
XX
SQ   Sequence  108 AA;

Query Match             82.7%;  Score 465;  DB 17;  Length 108;
Best Local Similarity   81.1%;  Pred. No. 4.1e-29;
Matches   86;  Conservative   10;  Mismatches   10;  Indels   0;  Gaps   0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||:||||||||||| :||||| :|||||||||||:||| |||||:|||| |||||||
Db    1 DIQLTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHEPGKGPRLLIRYTSKLESGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||||:|:||||:||||||||||||| ||:|||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYNLWTFGGGTKLEIK 106

RESULT 15
AAR06252
ID   AAR06252 standard; protein; 128 AA.
XX
AC   AAR06252;
XX
DT   10-DEC-1990 (first entry)
XX
DE   Variable region of murine AHT 107 light chain.
XX
KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
XX
PF   24-JAN-1990;  90EP-0101351.
XX
PR   04-DEC-1989;  89US-0441702.
PR   24-JAN-1989;  89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zerler B;
XX
DR   WPI; 1990-232892/31.
DR   N-PSDB; AAQ05556.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
```

PS   Disclosure; ; p; English.
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence   128 AA;

Query Match   81.9%;   Score 460.5; DB 11; Length 128;
Best Local Similarity 76.6%;   Pred. No. 1.1e-28;
Matches   82; Conservative 18; Mismatches   6; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||| :||:||||||||||||: :||| |: |||:|||| ||||||
Db   21 DIQMTQSPSSLSASLGGKVTLTCKTSQDINKFIAWYQHKPGEGPRLLIHYTSTLQPGIPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         ||||||||:|:|:|:||||||||||||||:|| |||| ||:|:|::
Db   81 RFSGSGSGKDYSFSINNLEPEDIATYYCLRYDDLPWTFGGGTKLEVR 127

Search completed: January 6, 2003, 13:15:17
Job time : 25.6263 secs

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                  GenCore version 5.1.3
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        January  6, 2003, 13:13:21 ; Search time 8.7798 Seconds
                                 (without alignments)
                                 355.228 Million cell updates/sec

Title:         US-09-155-739-7
Perfect score: 562
Sequence:      1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:      262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_AA:*
              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
              2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
              3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
              4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
              5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	2	US-08-561-521-7	Sequence 7, Appli
2	562	100.0	106	5	PCT-US95-01219-7	Sequence 7, Appli
3	508	90.4	106	2	US-08-561-521-5	Sequence 5, Appli
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appli
5	508	90.4	126	2	US-08-561-521-15	Sequence 15, Appli
6	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appli
7	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appli
8	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appli
9	481	85.6	128	1	US-08-339-582-4	Sequence 4, Appli
10	471.5	83.9	107	2	US-08-888-366-22	Sequence 22, Appli
11	460	81.9	637	1	US-08-235-838-16	Sequence 16, Appli
12	460	81.9	637	2	US-08-465-473B-16	Sequence 16, Appli
13	455	81.0	241	2	US-08-235-838-11	Sequence 11, Appli
14	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appli
15	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appli
16	453.5	80.7	107	5	US-08-561-521-8	Sequence 8, Appli
17	453.5	80.7	107	5	PCT-US95-01219-8	Sequence 8, Appli
18	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appli
19	448.5	79.8	107	3	US-07-934-373C-17	Sequence 17, Appli
20	448.5	79.8	107	4	US-08-437-642B-17	Sequence 17, Appli
21	448.5	79.8	107	4	US-08-146-206C-17	Sequence 17, Appli
22	448.5	79.8	107	5	PCT-US93-07832-17	Sequence 17, Appli
23	444.5	79.1	107	5	US-07-934-373C-18	Sequence 18, Appli
24	444.5	79.1	107	4	US-08-437-642B-18	Sequence 18, Appli
25	444.5	79.1	107	4	US-08-146-206C-18	Sequence 18, Appli
26	444.5	79.1	107	5	PCT-US93-07832-18	Sequence 18, Appli
27	444.5	79.1	108	3	US-08-974-899-3	Sequence 3, Appli
28	444.5	79.1	111	1	US-08-137-117D-67	Sequence 67, Appl
29	444.5	79.1	111	1	US-08-436-717-67	Sequence 67, Appl
30	444.5	79.1	126	1	US-08-137-117D-71	Sequence 71, Appl
31	444.5	79.1	126	2	US-08-436-717-71	Sequence 71, Appl
32	443.5	78.9	107	2	US-08-561-521-6	Sequence 6, Appli
33	443.5	78.9	107	2	US-08-652-558-34	Sequence 34, Appl
34	443.5	78.9	107	4	US-09-025-203-15	Sequence 15, Appl
35	443.5	78.9	107	5	PCT-US95-01219-6	Sequence 6, Appli
36	443.5	78.9	108	2	US-08-070-116A-7	Sequence 7, Appli
37	443.5	78.9	108	2	US-08-116-247-9	Sequence 9, Appli
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40	440.5	78.4	109	3	US-07-934-373C-3	Sequence 3, Appli
41	440.5	78.4	109	4	US-08-437-642B-3	Sequence 3, Appli
42	440.5	78.4	109	4	US-08-146-206C-3	Sequence 3, Appli
43	440.5	78.4	109	5	PCT-US93-07832-3	Sequence 3, Appli
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                            ALIGNMENTS

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RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;  APPLICANT: Bendig, Mary M.
;  APPLICANT: Leger, Olivier J.
;  APPLICANT: Saldanha, Jose
;  APPLICANT: Jones, S. Tarran
;  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;  TITLE OF INVENTION: Adhesion Molecule VLA-4
;  NUMBER OF SEQUENCES: 45
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
;  INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 106 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-561-521-7

  Query Match             100.0%;  Score 562;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-45;
  Matches  106;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 2
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-7

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Query Match             100.0%;  Score 562;  DB 5;  Length 106;
Best Local Similarity   100.0%;  Pred. No. 1.2e-45;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 3
US-08-561-521-5
; Sequence 5, Application US/08561521
; Patent No. 5840299

GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-5

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Query Match             90.4%;  Score 508;  DB 2;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 1.3e-40;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db  61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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RESULT 4
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

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; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-5

Query Match            90.4%;    Score 508;  DB 5;  Length 106;
Best Local Similarity  88.7%;    Pred. No. 1.3e-40;
Matches    94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db    1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

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Db   61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106

RESULT 5
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994


; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-2

Query Match            90.4%;    Score 508;  DB 2;  Length 126;
Best Local Similarity  88.7%;    Pred. No. 1.6e-40;
Matches    94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

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Db   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126

RESULT 6
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-15
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Query Match   90.4%; Score 508; DB 2; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.6e-40;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

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Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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RESULT 7
PCT-US95-01219-2
; Sequence 2, Application PC/TUS9501219
;   GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-2

Query Match   90.4%; Score 508; DB 5; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.6e-40;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

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Db   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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RESULT 8

PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
;   GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-15

Query Match   90.4%; Score 508; DB 5; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.6e-40;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

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Db   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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RESULT 9
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
;   GENERAL INFORMATION:
;   APPLICANT: Bigner, Darell D.
;   APPLICANT: Zalutsky, Michael R.
;   APPLICANT: Carrel, Stefan
;   TITLE OF INVENTION: METHOD OF TREATMENT
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Kenneth D. Sibley
;   STREET: P.O. Drawer 34009
;   CITY: Charlotte
;   STATE: No. 5558852th Carolina
;   COUNTRY: USA

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;       ZIP: 28234
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/339,582
;       FILING DATE:
;       CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/033,864
;       FILING DATE: 19-MAR-1993
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Sibley, Kenneth D.
;       REGISTRATION NUMBER: 31,665
;       REFERENCE/DOCKET NUMBER: 5405-89
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 919-420-2200
;       TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 128 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-339-582-4

Query Match    85.6%;   Score 481;   DB 1;   Length 128;
Best Local Similarity 84.0%;   Pred. No. 5.3e-38;
Matches   89;  Conservative   9;  Mismatches   8;  Indels   0;  Gaps   0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db     21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHPGKGPRLLMHYTSTLQPGIPS 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db     81 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGGTKLEIK 126

RESULT 10
US-08-888-366-22
; Sequence 22, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
;     APPLICANT: Lopez, Osvaldo
;     APPLICANT: Wylie, Dwane E.
;     APPLICANT: Wagner, Fred W.
;     TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
;     NUMBER OF SEQUENCES: 39
;     CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Merchant & Gould
;     STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55402
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/888,366
;       FILING DATE: 03-JUL-1997
;       CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/187,407
;       FILING DATE: 27-JAN-1994
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/990,542
;       FILING DATE: 14-DEC-1992
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;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/493,299
;       FILING DATE: 14-MAR-1990
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/324,392
;       FILING DATE: 14-MAR-1989
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Carter, Charles G.
;       REGISTRATION NUMBER: 35,093
;       REFERENCE/DOCKET NUMBER: 8648.39USC1
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 612-332-5300
;       TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 107 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-366-22

Query Match    83.9%;   Score 471.5;   DB 2;   Length 107;
Best Local Similarity 83.2%;   Pred. No. 3.4e-37;
Matches   89;  Conservative   9;  Mismatches   8;  Indels   1;  Gaps   1;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db      1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHPGKGPRLLIHYTSTLQPGIPS 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
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Db     61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107

RESULT 11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
;     APPLICANT: Wels, Winfried S.
;     APPLICANT: Hynes, Nancy E.
;     APPLICANT: Hatwerth, Ina-Maria
;     APPLICANT: Groner, Bernd
;     APPLICANT: Hardman, No. 5571894man
;     APPLICANT: Zwickl, Markus
;     TITLE OF INVENTION: Recombinant Antibodies Specific for a
;     TITLE OF INVENTION: Growth Factor Receptor
;     NUMBER OF SEQUENCES: 16
;     CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CIBA-GEIGY Corporation
;     STREET: 7 Skyline Drive
;     CITY: Hawthorne
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10532
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/235,838
;       FILING DATE: TBA
;       CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/828,832
;       FILING DATE: 31-JAN-1992
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: GB 91-810079.3
;       FILING DATE: 05-FEB-1991
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Elmer, James Scott
;       REGISTRATION NUMBER: 36,129
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;       REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (919)541-8614
;          TELEFAX:  (919)541-8689
; INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 637 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-235-838-16

Query Match      81.9%;  Score 460;  DB 1;  Length 637;
Best Local Similarity   80.2%;  Pred. No. 2.8e-35;
Matches  85;  Conservative  10;  Mismatches  11;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db  168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||||:|:::|:::||||||||| | |:||||:||||:|||
Db  228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273

RESULT 12
US-08-465-473B-16
; Sequence 16, Application US/08465473B
; Patent No. 5939531
GENERAL INFORMATION:
;       APPLICANT: Wels, Winfried S.
;       APPLICANT: Hynes, Nancy E.
;       APPLICANT: Harwerth, Ina-Maria
;       APPLICANT: Groner, Bernd
;       APPLICANT: Hardman, No. 5939531man
;       APPLICANT: Zwickl, Markus
;       TITLE OF INVENTION: Recombinant Antibodies Specific for a
;       TITLE OF INVENTION: Growth Factor Receptor
;       NUMBER OF SEQUENCES: 34
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: NOVARTIS Corporation
;          STREET: 564 Morris Avenue
;          CITY: Summit
;          STATE: New Jersey
;          COUNTRY: USA
;          ZIP: 07901-6940
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/465,473B
;          FILING DATE: 5 June 1995
;          CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 07/828,832
;          FILING DATE: 31-JAN-1992
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: GB 91-810079.3
;          FILING DATE: 05-FEB-1991
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Pfeiffer, Hesna J.
;          REGISTRATION NUMBER: 22,640
;          REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (908)522 6940
;          TELEFAX:  (908)522 6955
; INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 637 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
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;       MOLECULE TYPE: protein
US-08-465-473B-16

Query Match      81.9%;  Score 460;  DB 2;  Length 637;
Best Local Similarity   80.2%;  Pred. No. 2.8e-35;
Matches  85;  Conservative  10;  Mismatches  11;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db  168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db  228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273

RESULT 13
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
GENERAL INFORMATION:
;       APPLICANT: Wels, Winfried S.
;       APPLICANT: Hynes, Nancy E.
;       APPLICANT: Harwerth, Ina-Maria
;       APPLICANT: Groner, Bernd
;       APPLICANT: Hardman, No. 5571894man
;       APPLICANT: Zwicki, Markus
;       TITLE OF INVENTION: Recombinant Antibodies Specific for a
;       TITLE OF INVENTION: Growth Factor Receptor
;       NUMBER OF SEQUENCES: 16
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: CIBA-GEIGY Corporation
;          STREET: 7 Skyline Drive
;          CITY: Hawthorne
;          STATE: New York
;          COUNTRY: USA
;          ZIP: 10532
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/235,838
;          FILING DATE: TBA
;          CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 07/828,832
;          FILING DATE: 31-JAN-1992
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: GB 91-810079.3
;          FILING DATE: 05-FEB-1991
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Elmer, James Scott
;          REGISTRATION NUMBER: 36,129
;          REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (919)541-8614
;          TELEFAX:  (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 241 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-235-838-11

Query Match      81.0%;  Score 455;  DB 1;  Length 241;
Best Local Similarity   80.0%;  Pred. No. 2.8e-35;
Matches  84;  Conservative  10;  Mismatches  11;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db   137 DIQLTQSPSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196
Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
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Db   197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
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RESULT 14
US-08-465-473B-11
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; Sequence 11, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
;    APPLICANT: Wels, Winfried S.
;    APPLICANT: Hynes, Nancy E.
;    APPLICANT: Harwerth, Ina-Maria
;    APPLICANT: Groner, Bernd
;    APPLICANT: Hardman, No. 5939531man
;    APPLICANT: Zwickl, Markus
;    TITLE OF INVENTION: Recombinant Antibodies Specific for a
;    TITLE OF INVENTION: Growth Factor Receptor
;    NUMBER OF SEQUENCES: 34
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE: NOVARTIS Corporation
;    STREET: 564 Morris Avenue
;    CITY: Summit
;    STATE: New Jersey
;    COUNTRY: USA
;    ZIP: 07901-6940
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/465,473B
;    FILING DATE: 5 June 1995
;    CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 07/828,832
;    FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: GB 91-810079.3
;    FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
;    NAME: Pfeiffer, Hesna J.
;    REGISTRATION NUMBER: 22,640
;    REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (908)522 6940
;    TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 11:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 241 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: Protein
US-08-465-473B-11

Query Match             81.0%;  Score 455;  DB 2;  Length 241;
Best Local Similarity   80.0%;  Pred. No. 2.8e-35;
Matches  84;  Conservative  10;  Mismatches  11;  Indels  0;  Gaps  0;

Qy     1 DIQMTQSPSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db   137 DIQLTQSPSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196

Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
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Db   197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
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RESULT 15
US-08-602-725-29

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; Sequence 29, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
;    APPLICANT: BODMER, WALTER F
;    APPLICANT: DURBIN, HELGA
;    APPLICANT: SNARY, DAVID
;    APPLICANT: STEWART, LORNA MD
;    APPLICANT: YOUNG, SUSAN
;    APPLICANT: BATES, PAUL A
;    TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES: 40
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE: NIXON & VANDERHYE P.C.
;    STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;    CITY: ARLINGTON
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22201
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/602,725
;    FILING DATE: 02-FEB-1996
;    CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: PCT/GB94/01816
;    FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: GB 9317423
;    FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
;    NAME: SADOFF, B.J.
;    REGISTRATION NUMBER: 36663
;    REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-816-4091
;    TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 29:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 108 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
;    MOLECULE TYPE: peptide
;    HYPOTHETICAL: NO
;    FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
;    ORGANISM: Hukan REI light chain
US-08-602-725-29

Query Match             80.9%;  Score 454.5;  DB 2;  Length 108;
Best Local Similarity   83.0%;  Pred. No. 1.3e-35;
Matches  88;  Conservative  8;  Mismatches  9;  Indels  1;  Gaps  1;

Qy     1 DIQMTQSPSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
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Job time : 9.7798 secs
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  January  6, 2003, 13:17:36 ; Search time 5.13939 Seconds
                                       (without alignments)
                                     390.875 Million cell updates/sec

Title:          US-09-155-739-7
Perfect score:  562
Sequence:       1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters:        117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA:*
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            6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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           13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	479.5	85.3	108	10	US-09-229-200A-11	Sequence 11, Appl
2	479.5	85.3	108	10	US-09-229-200A-15	Sequence 15, Appl
3	466.5	83.0	108	10	US-09-229-200A-16	Sequence 16, Appl
4	449.5	80.0	107	10	US-09-056-160B-15	Sequence 15, Appl
5	446.5	79.4	110	10	US-09-056-160B-103	Sequence 103, App
6	446.5	79.4	237	10	US-09-056-160B-100	Sequence 100, App
7	446.5	79.4	491	12	US-10-011-125-2	Sequence 2, Appli
8	445.5	79.3	107	10	US-09-056-160B-13	Sequence 13, Appl
9	444.5	79.1	108	10	US-09-056-160B-12	Sequence 12, Appl
10	444.5	79.1	109	10	US-09-811-123-6	Sequence 6, Appli
11	443.5	78.9	107	9	US-09-999-025-15	Sequence 15, Appl
12	443.5	78.9	107	9	US-09-999-040-15	Sequence 15, Appl
13	443.5	78.9	108	10	US-09-229-200A-14	Sequence 14, Appl
14	443.5	78.9	110	10	US-09-056-160B-105	Sequence 105, App
15	443	78.8	109	10	US-09-229-200A-7	Sequence 7, Appli
16	442.5	78.7	108	9	US-10-153-159-2	Sequence 2, Appli
17	442.5	78.7	108	9	US-10-153-159-16	Sequence 16, Appl
18	442.5	78.7	108	10	US-09-056-160B-8	Sequence 8, Appli
19	441.5	78.6	107	10	US-09-253-794-6	Sequence 6, Appli
20	439.5	78.2	108	9	US-10-153-159-4	Sequence 4, Appli
21	439.5	78.2	110	10	US-09-056-160B-107	Sequence 107, App
22	439.5	78.2	110	10	US-09-056-160B-117	Sequence 117, App
23	438.5	78.0	108	10	US-09-905-243-73	Sequence 73, Appl
24	438.5	78.0	127	10	US-09-809-739-10	Sequence 10, Appl
25	438.5	78.0	214	10	US-09-940-166A-2	Sequence 2, Appli
26	438.5	78.0	214	10	US-09-811-384-11	Sequence 11, Appl
27	438.5	78.0	237	10	US-09-940-166A-6	Sequence 6, Appli
28	436.5	77.7	108	10	US-09-056-160B-126	Sequence 126, App
29	435.5	77.5	108	10	US-09-229-200A-17	Sequence 17, Appl
30	432.5	77.0	263	10	US-09-956-086-3	Sequence 3, Appli
31	432.5	77.0	263	9	US-09-956-087-3	Sequence 3, Appli
32	432.5	77.0	283	9	US-09-985-442-6	Sequence 6, Appli
33	432.5	77.0	283	10	US-09-983-580-6	Sequence 19, Appl
34	430	76.5	106	10	US-09-253-794-19	Sequence 6, Appli
35	430	76.5	232	9	US-10-006-771A-6	Sequence 2, Appli
36	430	76.5	443	10	US-10-006-771A-2	Sequence 109, App
37	430	76.5	443	9	US-10-006-773-2	Sequence 111, App
38	427.5	76.1	110	12	US-09-056-160B-109	Sequence 113, App
39	427.5	76.1	110	10	US-09-056-160B-111	Sequence 115, App
40	427.5	76.1	110	10	US-09-056-160B-113	Sequence 6, Appli
41	427.5	76.1	110	10	US-09-056-160B-115	Sequence 6, Appli
42	425.5	75.7	126	10	US-09-760-723-6	Sequence 30, Appl
43	425.5	75.7	126	10	US-09-355-925-6	Sequence 6, Appli
44	425.5	75.7	236	10	US-09-859-053-30	
45	425.5	75.7	245	9	US-09-797-941A-6	

ALIGNMENTS

```
RESULT 1
US-09-229-200A-11
; Sequence 11, Application US/09229200A
; Patent No. US2002009179A1
GENERAL INFORMATION:
   APPLICANT: Jolliffe et al.
   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
   NUMBER OF SEQUENCES: 28
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Johnson & Johnson
      STREET: One Johnson & Johnson Plaza
      CITY: New Brunswick
      STATE: NJ
      COUNTRY: USA
      ZIP: 08933-7003
   COMPUTER READABLE FORM:
      MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
      COMPUTER: IBM
      OPERATING SYSTEM: PC-DOS
      SOFTWARE: <Unknown>
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/229,200A
      FILING DATE: 13-Jan-1999
      CLASSIFICATION: <Unknown>
   ATTORNEY/AGENT INFORMATION:
      NAME: John W. Wallen, III
      REGISTRATION NUMBER: 35,403
      REFERENCE/DOCKET NUMBER: ORT-948
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (858) 784-3239
      TELEFAX: (908) 524-2808
   INFORMATION FOR SEQ ID NO: 11:
      SEQUENCE CHARACTERISTICS:
         LENGTH: 108
         TYPE: amino acid
         TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 11:
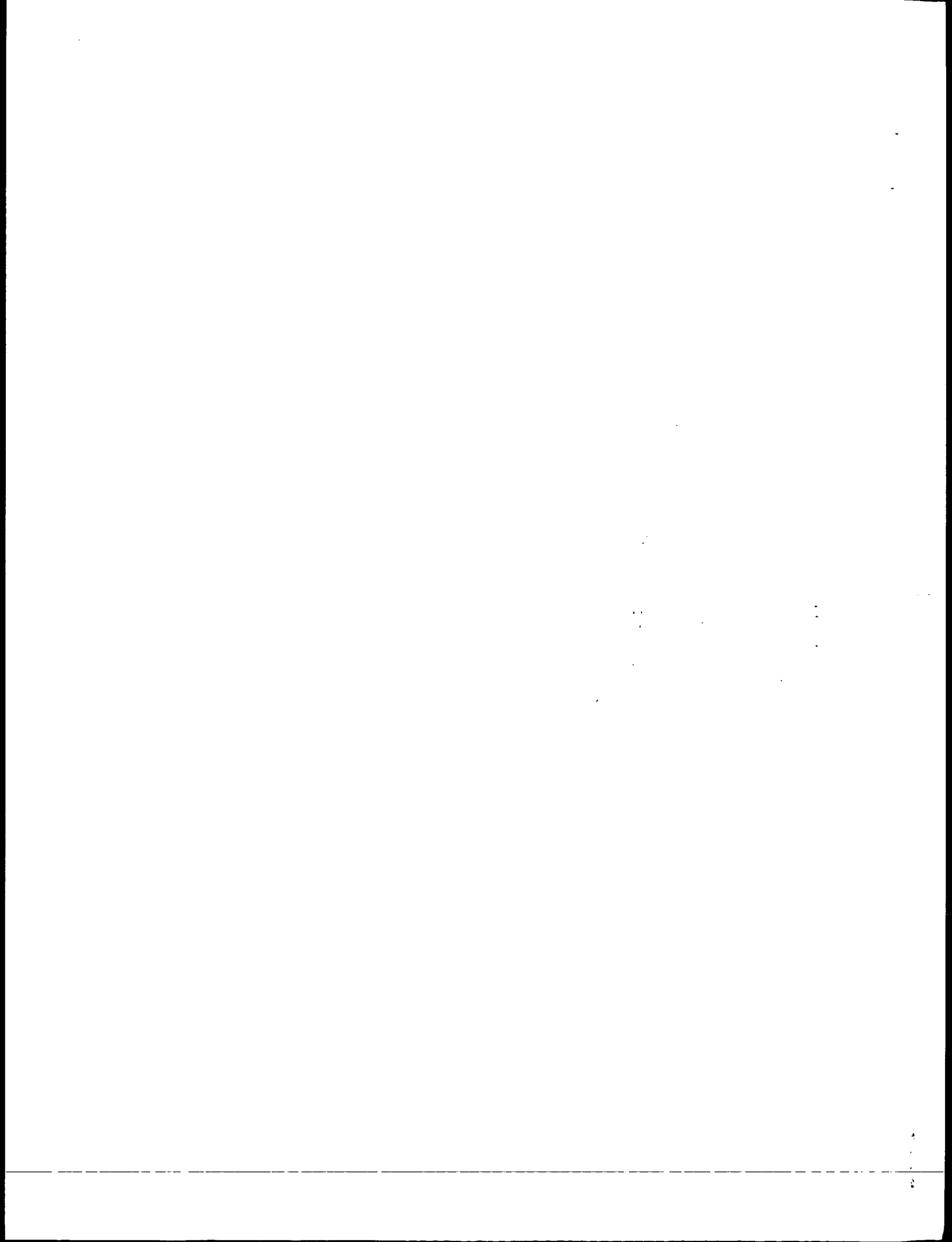US-09-229-200A-11

  Query Match             85.3%;  Score 479.5;  DB 10;  Length 108;
  Best Local Similarity   85.8%;  Pred. No. 1e-28;
  Matches   91;  Conservative    7;  Mismatches    7;  Indels    1;  Gaps    1;
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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||||    |: |||||||||||||| ||||||:|
Db    1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          |||||||| |||||||||||||||||| :||||||:|||||||||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYDNLIFTFGGGTKLQI 106
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RESULT 2
US-09-229-200A-15
; Sequence 15, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 15
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-229-200A-15

Query Match   85.3%; Score 479.5; DB 10; Length 108;
Best Local Similarity   85.8%; Pred. No. 1e-28;
Matches 91; Conservative   7; Mismatches   7; Indels   1; Gaps   1;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||||    |: |||||||||||||| ||||||:|
Db    1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          |||||||| |||||||||||||||||| :||||||:|||||||||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYDNLIFTFGGGTKLQI 106
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RESULT 3
US-09-229-200A-16
; Sequence 16, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 16
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16
US-09-229-200A-16

Query Match   83.0%; Score 466.5; DB 10; Length 108;
Best Local Similarity   84.9%; Pred. No. 8.8e-28;
Matches 90; Conservative   6; Mismatches   9; Indels   1; Gaps   1;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||||||||||:||||||:|||||||||||||| ||||:|
Db    1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYIAWYQHTPGKAPKLLIHYTSTLQPGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          |||||||| |||||||||||||||| |||:||:|||||||||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYCLQYDNLIFTFGGGTKLQI 106
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RESULT 4
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
;   APPLICANT: Baca, Manuel
;   APPLICANT: Wells, James A.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Chen, Yvonne M.
;   TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;   NUMBER OF SEQUENCES: 131
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/056,160B
;   FILING DATE: 06-Apr-1998
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/054,856
;   FILING DATE: 06-AUG-1997
;   ATTORNEY/AGENT INFORMATION:

```
          NAME: Hasak, Janet E.
          REGISTRATION NUMBER: 28,616
          REFERENCE/DOCKET NUMBER: P1093R2
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: 650/225-1896
          TELEFAX: 650/952-9881
      INFORMATION FOR SEQ ID NO: 15:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 107 amino acids
          TYPE: Amino Acid
          TOPOLOGY: Linear
US-09-056-160B-15

Query Match             80.0%;  Score 449.5;  DB 10;  Length 107;
  Best Local Similarity   79.4%;  Pred. No. 1.5e-26;
  Matches   85;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||||||||||||| ||||  |  |||| :  ||| ||||||:||:| :|:||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              |||||||| |||  ||||||||||| :: ||||||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107

RESULT 5
US-09-056-160B-103
; Sequence 103, Application US/09056160B
; Patent No. US2002032315A1
; GENERAL INFORMATION:
;   APPLICANT:  Baca, Manuel
;   APPLICANT:  Wells, James A.
;   APPLICANT:  Presta, Leonard G.
;   APPLICANT:  Lowman, Henry B.
;   APPLICANT:  Chen, Yvonne M.
;   TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;   NUMBER OF SEQUENCES: 131
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET:  1 DNA Way
;     CITY:   South San Francisco
;     STATE:   California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/056,160B
;     FILING DATE:  06-Apr-1998
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/054,856
;     FILING DATE:  06-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hasak, Janet E.
;     REGISTRATION NUMBER: 28,616
;     REFERENCE/DOCKET NUMBER: P1093R2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650/225-1896
;     TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 110 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
US-09-056-160B-103

Query Match             79.4%;  Score 446.5;  DB 10;  Length 110;
  Best Local Similarity   78.5%;  Pred. No. 2.5e-26;
  Matches   84;  Conservative    9;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||:|||||||||||||||||| ||||  |  |||| :  ||| ||||||:||:| :|:||
Db          1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              |||||||| |||  ||||||||||| :: ||||||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107

RESULT 6
US-09-056-160B-100
; Sequence 100, Application US/09056160B
; Patent No. US2002032315A1
; GENERAL INFORMATION:
;   APPLICANT:  Baca, Manuel
;   APPLICANT:  Wells, James A.
;   APPLICANT:  Presta, Leonard G.
;   APPLICANT:  Lowman, Henry B.
;   APPLICANT:  Chen, Yvonne M.
;   TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;   NUMBER OF SEQUENCES: 131
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET:  1 DNA Way
;     CITY:   South San Francisco
;     STATE:   California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/056,160B
;     FILING DATE:  06-Apr-1998
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/054,856
;     FILING DATE:  06-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hasak, Janet E.
;     REGISTRATION NUMBER: 28,616
;     REFERENCE/DOCKET NUMBER: P1093R2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650/225-1896
;     TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 237 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
US-09-056-160B-100

Query Match             79.4%;  Score 446.5;  DB 10;  Length 237;
  Best Local Similarity   78.5%;  Pred. No. 4.6e-26;
  Matches   84;  Conservative    9;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||:|||||||||||||||||| ||||  |  |||| :  ||| ||||||:||:| :|:||
Db         24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              |||||||| |||  ||||||||||| :: ||||||||||||||||||
Db         84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 130

RESULT 7
US-10-011-125-2
; Sequence 2, Application US/10011125
; Patent No. US20020142388A1
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; GENERAL INFORMATION:
;   APPLICANT: Chen, Christina Yu-Ching
;   TITLE OF INVENTION: BACTERIAL HOST STRAINS
;   FILE REFERENCE: P1804R1
;   CURRENT APPLICATION NUMBER: US/10/011,125
;   CURRENT FILING DATE: 2001-12-07
;   PRIOR APPLICATION NUMBER: US 60/256,162
;   PRIOR FILING DATE: 2000-12-14
;   NUMBER OF SEQ ID NOS: 10
;   SEQ ID NO 2
;     LENGTH: 491
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

Query Match             79.4%;  Score 446.5;  DB 12;  Length 491;
Best Local Similarity   78.5%;  Pred. No. 8.3e-26;
Matches   84;  Conservative    9;  Mismatches  13;  Indels   1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||||||||||| : |||:|  ||||:: ||||:||:||:||  :  ||:|
Db         24 DIQLTQSPSSLSASVGDRVTITCCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              ||||||  |||  ||||||||||||  : ||||||||||||||
Db         84 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 130

RESULT 8
US-09-056-160B-13
;   Sequence 13, Application US/09056160B
;   Patent No. US2002003231SA1
; GENERAL INFORMATION:
;   APPLICANT: Baca, Manuel
;   APPLICANT: Wells, James A.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Chen, Yvonne M.
;   TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;   NUMBER OF SEQUENCES: 131
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  1 DNA Way
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/056,160B
;     FILING DATE:  06-Apr-1998
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/054,856
;     FILING DATE:  06-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Hasak, Janet E.
;     REGISTRATION NUMBER:  28,616
;     REFERENCE/DOCKET NUMBER:  P1093R2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650/225-1896
;     TELEFAX:  650/952-9881
; INFORMATION FOR SEQ ID NO:  13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  107 amino acids
;     TYPE:  Amino Acid
;     TOPOLOGY:  Linear
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US-09-056-160B-13

Query Match             79.3%;  Score 445.5;  DB 10;  Length 107;
Best Local Similarity   78.5%;  Pred. No. 2.9e-26;
Matches   84;  Conservative    9;  Mismatches  13;  Indels   1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||||||||||| : |||:|  ||||:: ||||:||:||:||  :  ||:|
Db          1 DIQMTQSPSSLSASVGDRVTITCCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              ||||||  |||  : |||||||||||||  : ||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107

RESULT 9
US-09-056-160B-12
;   Sequence 12, Application US/09056160B
;   Patent No. US2002003231SA1
; GENERAL INFORMATION:
;   APPLICANT: Baca, Manuel
;   APPLICANT: Wells, James A.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Chen, Yvonne M.
;   TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;   NUMBER OF SEQUENCES: 131
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  1 DNA Way
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/056,160B
;     FILING DATE:  06-Apr-1998
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/054,856
;     FILING DATE:  06-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Hasak, Janet E.
;     REGISTRATION NUMBER:  28,616
;     REFERENCE/DOCKET NUMBER:  P1093R2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650/225-1896
;     TELEFAX:  650/952-9881
; INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  108 amino acids
;     TYPE:  Amino Acid
;     TOPOLOGY:  Linear
US-09-056-160B-12

Query Match             79.1%;  Score 444.5;  DB 10;  Length 108;
Best Local Similarity   78.5%;  Pred. No. 3.4e-26;
Matches   84;  Conservative   11;  Mismatches  11;  Indels   1;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||||||||||| : |||:|  ||||:: ||||:||:||:|| |:  ||:|
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              ||||||  |||  ||||||||||||  : ||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
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RESULT 10
US-09-811-123-6
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6

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Query Match       79.1%;  Score 444.5; DB 10; Length 109;
Best Local Similarity 78.5%;  Pred. No. 3.4e-26;
Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||| |: | :||||:|||||::||: : :|: :||
Db  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||| |:|||||||||| |||| ||::|  ||||||||||
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
```

RESULT 11
US-09-999-025-15
; Sequence 15, Application US/09999025
; Publication NO. US20020183497A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,025
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 15
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: REI VL
; LOCATION: 1..107
US-09-999-025-15

```
Query Match       78.9%;  Score 443.5; DB 9; Length 107;
Best Local Similarity 81.1%;  Pred. No. 4e-26;
Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||| ||: |||||||||||||||||||||:||
Db  1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
        ||||||| |||||||||||||||||||||| |: | :|||||||||:
Db 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
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RESULT 12
US-09-999-040-15
; Sequence 15, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 15
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: REI VL
; LOCATION: 1..107
US-09-999-040-15

```
Query Match       78.9%;  Score 443.5; DB 9; Length 107;
Best Local Similarity 81.1%;  Pred. No. 4e-26;
Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||| ||: |||||||||||||||||||||:||
Db  1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
        ||||||| |||||||||||||||||||||| |: | :|||||||||:
Db 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
```

RESULT 13
US-09-229-200A-14
; Sequence 14, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:

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                MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                COMPUTER: IBM
                OPERATING SYSTEM: PC-DOS
                SOFTWARE: <Unknown>
           CURRENT APPLICATION DATA:
                APPLICATION NUMBER: US/09/229,200A
                FILING DATE: 13-Jan-1999
                CLASSIFICATION: <Unknown>
           ATTORNEY/AGENT INFORMATION:
                NAME: John W. Wallen, III
                REGISTRATION NUMBER: 35,403
                REFERENCE/DOCKET NUMBER: ORT-948
           TELECOMMUNICATION INFORMATION:
                TELEPHONE: (858) 784-3239
                TELEFAX: (908) 524-2808
      INFORMATION FOR SEQ ID NO: 14:
           SEQUENCE CHARACTERISTICS:
                LENGTH: 108
                TYPE: amino acid
                TOPOLOGY: linear
           SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-229-200A-14

Query Match      78.9%;     Score 443.5;  DB 10;  Length 108;
Best Local Similarity 81.1%;  Pred. No. 4e-26;
Matches   86;  Conservative   9;  Mismatches  10;  Indels    1;  Gaps    1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       ||||||||||||||||||||||| ||  ||| || | : |||||||||||: :|||:
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
       |||||| |||||||||||||||||||||| :  :  :||||||||:|
Db  61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
```

RESULT 14
US-09-056-160B-105
; Sequence 105, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
     APPLICANT: Baca, Manuel
     APPLICANT: Wells, James A.
     APPLICANT: Presta, Leonard G.
     APPLICANT: Lowman, Henry B.
     APPLICANT: Chen, Yvonne M.
     TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
     NUMBER OF SEQUENCES: 131
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Genentech, Inc.
          STREET: 1 DNA Way
          CITY: South San Francisco
          STATE: California
          COUNTRY: USA
          ZIP: 94080
     COMPUTER READABLE FORM:
          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: WinPatin (Genentech)
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/056,160B
          FILING DATE: 06-Apr-1998
          CLASSIFICATION: 424
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 60/054,856
          FILING DATE: 06-AUG-1997
     ATTORNEY/AGENT INFORMATION:
          NAME: Hasak, Janet E.
          REGISTRATION NUMBER: 28,616
          REFERENCE/DOCKET NUMBER: P1093R2
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 650/225-1896
          TELEFAX: 650/952-9881
     INFORMATION FOR SEQ ID NO: 105:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 110 amino acids
               TYPE: Amino Acid
               TOPOLOGY: Linear
US-09-056-160B-105

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Query Match      78.9%;     Score 443.5;  DB 10;  Length 110;
Best Local Similarity 77.6%;  Pred. No. 4.1e-26;
Matches   83;  Conservative  10;  Mismatches  13;  Indels   13;  Gaps    1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||:||||||||||||||||||| ||| : | : ||||||||| |::|| :::|||:||
Db   1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
       |||||||| ||||:||||||||| |||||| : : ::||||||||||
Db  61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107
```

RESULT 15
US-09-229-200A-7
; Sequence 7, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
     APPLICANT: Jolliffe et al.
     TITLE OF INVENTION: CD4 Specific Recombinant Antibody
     NUMBER OF SEQUENCES: 28
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Johnson & Johnson
          STREET: One Johnson & Johnson Plaza
          CITY: New Brunswick
          STATE: NJ
          COUNTRY: USA
          ZIP: 08933-7003
     COMPUTER READABLE FORM:
          MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
          COMPUTER: IBM
          OPERATING SYSTEM: PC-DOS
          SOFTWARE: <Unknown>
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/229,200A
          FILING DATE: 13-Jan-1999
          CLASSIFICATION: <Unknown>
     ATTORNEY/AGENT INFORMATION:
          NAME: John W. Wallen, III
          REGISTRATION NUMBER: 35,403
          REFERENCE/DOCKET NUMBER: ORT-948
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (858) 784-3239
          TELEFAX: (908) 524-2808
     INFORMATION FOR SEQ ID NO: 7:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 109
               TYPE: amino acid
               TOPOLOGY: linear
          SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-200A-7

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Query Match      78.8%;     Score 443;  DB 10;  Length 109;
Best Local Similarity 76.9%;  Pred. No. 4.4e-26;
Matches   83;  Conservative  14;  Mismatches   9;  Indels    2;  Gaps    1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||| :||  :|| |: ||| ::| :||||:|| ||||:| ::||||||
Db   1 DIQMTQSPSSLSASLGGKVTIACKASQDINNYIAWYQHKPGKGPRLLIYHTSTLQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
       |||||||||||:|:: ||||||||||||::|: :|  ||| ||||:||
Db  61 RFSGSGSGRDYSFSINLEPEDIATYYCIQYNDLFLTTFGGGTKLEIK 108
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us-09-155-739-7.rapb

Mon Jan 6 14:19:48 2003

Search completed: January 6, 2003, 13:29:31
Job time : 5.13939 secs

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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      January   6, 2003, 13:12:26 ; Search time 9.85051 Seconds
                                           (without alignments)
                                           1034.490 Million cell updates/sec

Title:        US-09-155-739-7
Perfect score: 562
Sequence:     1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:          283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_73:*
              1:  pir1:*
              2:  pir2:*
              3:  pir3:*
              4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488	86.8	104	2	S26330	Ig kappa chain V r
2	479	85.2	104	2	S26329	Ig kappa chain V r
3	478	85.1	106	2	C33936	Ig kappa chain V r
4	463.5	82.5	125	2	S09365	Ig kappa chain - m
5	452	80.4	97	2	PH1064	Ig light chain V r
6	446.5	79.4	107	2	PL0270	Ig kappa chain V r
7	443.5	78.9	108	1	K1HURE	Ig kappa chain V-I
8	443.5	78.9	129	2	S52789	Ig kappa chain V r
9	443	78.8	103	2	S26332	Ig light chain V r
10	440.5	78.4	107	2	PL0272	Ig kappa chain V r
11	440	78.3	94	2	E33730	Ig kappa chain V r
12	439.5	78.2	107	2	PL0269	Ig kappa chain V r
13	439.5	78.2	107	2	PL0271	Ig kappa chain V-I
14	439.5	78.2	108	1	K1HUAU	Ig kappa chain (BR
15	435.5	77.5	108	2	I39154	Ig kappa chain V-J
16	429.5	76.4	110	2	S44118	Ig kappa chain V-J
17	429.5	76.4	127	2	S40367	Ig kappa chain V-J
18	426	75.8	107	2	S36275	Ig lambda chain V
19	424	75.5	125	2	S40333	Ig kappa chain V-J
20	421.5	75.0	108	1	K1HULY	Ig kappa chain V-I
21	419.5	74.6	108	1	K1HUAG	Ig kappa chain V-I
22	419.5	74.6	108	1	K1HURY	Ig kappa chain V-I
23	418.5	74.5	123	2	S40331	Ig kappa chain - h
24	415.5	73.9	109	2	S31998	Ig kappa chain V-J
25	414.5	73.8	131	2	S40352	Ig kappa chain V-J
26	414	73.7	124	2	S40336	Ig kappa chain V-J
27	413.5	73.6	108	1	K1HUSW	Ig kappa chain V-I
28	412.5	73.4	108	2	B49047	Ig kappa chain V r
29	412	73.3	106	2	PC2397	anti-tetanus toxin
30	410.5	73.0	108	2	S44122	Ig kappa chain V r
31	410.5	73.0	109	2	S31981	Ig kappa chain - h
32	409.5	72.9	129	1	K1HUWK	Ig kappa chain pre
33	409	72.8	107	1	K1HUAR	Ig kappa chain V-I
34	408.5	72.7	108	1	K1HUWE	Ig kappa chain V-I
35	408.5	72.7	139	2	S40365	Ig kappa chain - h
36	407.5	72.5	141	2	A49134	Ig kappa chain V-J
37	405.5	72.2	117	2	S46371	Ig kappa chain V-J
38	405	72.1	108	2	S30521	Ig kappa chain - h
39	404.5	72.0	132	2	S40334	Ig kappa chain V r
40	403.5	71.8	94	2	PH1063	Ig lambda chain V
41	403.5	71.8	107	2	S36264	Ig kappa chain V r
42	403.5	71.8	127	2	S11240	Ig kappa chain V r
43	403	71.7	117	2	S43528	Ig kappa chain V r
44	403	71.7	117	2	S42263	Ig kappa chain V r
45	402.5	71.6	108	1	K1HUHU	Ig kappa chain V-I

ALIGNMENTS

```
RESULT 1
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match             86.8%;  Score 488;  DB 2;  Length 104;
Best Local Similarity   85.6%;  Pred. No. 1.6e-35;
Matches   89;  Conservative   8;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||  |||||| :||||||  ||||||||  ||| |||||||||||| 60
Db     1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYCLQYDNLWTFGQGTKVE 104
           |||||||||||  :||||||||||||||||||||||||||:| 104
Db    61 RFSGSGSGRDYSFSISNLEPEDIATYCLQYDNLWTFGGGTKLE 104

RESULT 2
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match             85.2%;  Score 479;  DB 2;  Length 104;
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Best Local Similarity 84.6%; Pred. No. 9.8e-35; Indels 0; Gaps 0;
Matches 88; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||| ||:|||||| :|||||| ||| |||||||| |||||||| ||||||
Db 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
       ||||||||||:|:|:|| ||||||||||||||| |:|||:|||:
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLTFGGGTKLE 104

RESULT 3
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 478; DB 2; Length 106;
Best Local Similarity 83.0%; Pred. No. 1.2e-34;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||| ||:|||||| :|||||| ||| |||||||| |||||||| ||||||
Db 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
       ||||||||||:|:|:|| :||:||||||||||| |:|||:|||:||
Db 61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106

RESULT 4
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm
A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 463.5; DB 2; Length 125;
Best Local Similarity 83.2%; Pred. No. 2.5e-33;
Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||| ||:||||||-:|||||| ||| |||||||| |||||||| ||||||
Db 18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW-TFGQGTKVEIK 106
       |||||||| ||:|:|:|| ||||||||||||||| :|||:|||:||
Db 78 RFSGSGSGGDYSFSISNLGPEDIATYYCLQYDNLLRFGGGTKLEIK 124

RESULT 5
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 452; DB 2; Length 97;
Best Local Similarity 85.6%; Pred. No. 2e-32;
Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       |||||||||||||| ||:|||||| :|||||| ||| |||||||| |||||||| ||||||
Db 1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
       ||||||||||:|:|:|| :||:|||||||||||||:||
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97

RESULT 6
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:9011618; PMID:2104919
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match 79.4%; Score 446.5; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 6.4e-32;
Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       ||||||| .|||| | ||.|||| :|||.:|| |||||| | |||||||.||||||||||
Db 1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
       ||||||||||:|:|:|| :||:|||||||||| :|||:|||:||
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 7
K1HURE

Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom K
vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:76023758; PMID:809329
A;Accession: A91663
A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
A;Reference number: A90392; MUID:76039968; PMID:1182131
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

Query Match   78.9%; Score 443.5; DB 1; Length 108;
Best Local Similarity 81.1%; Pred. No. 1.2e-31;
Matches   86; Conservative   9; Mismatches 10; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||: ||| |||:|||| |:|: ||| |||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
        ||||||||| ||||||||||||||||||||| : ||||||||||:|
Db 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106

RESULT 8
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   78.9%; Score 443.5; DB 2; Length 129;
Best Local Similarity 79.4%; Pred. No. 1.4e-31;
Matches   85; Conservative 10; Mismatches 11; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||: ||| |||:|||| |:|: ||| ||||||| :|: :||
Db 23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||| ||||||||||||||||||||| : || || ||||||
Db 83 RFSGSGSGTDFSFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 129

RESULT 9
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   78.8%; Score 443; DB 2; Length 103;
Best Local Similarity 77.7%; Pred. No. 1.2e-31;
Matches   80; Conservative 13; Mismatches 10; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||| :|| || :|| |||:|||| || || |||||||| || ||||||||
Db   1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKV 103
        ||||||||||| : :||||||||||||||||||||:||||||:
Db 61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103

RESULT 10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   78.4%; Score 440.5; DB 2; Length 107;
Best Local Similarity 78.5%; Pred. No. 2.1e-31;
Matches   84; Conservative 11; Mismatches 11; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||| ::| |||||| :|| |||:|||| || || |||||||| |:| |||||||
Db   1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106

```
Db        61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 11
E33730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
A;Accession: E33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match             78.3%;  Score 440;  DB 2;  Length 94;
Best Local Similarity   86.2%;  Pred. No. 2.1e-31;
Matches   81;  Conservative    7;  Mismatches    6;    Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           | |||||||||||||:||:|  |||||| ||||||||| || ||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
           ||||||||||::||:||:||||||||||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94

RESULT 12
PL0269
Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match             78.2%;  Score 439.5;  DB 2;  Length 107;
Best Local Similarity   78.5%;  Pred. No. 2.6e-31;
Matches   84;  Conservative   10;  Mismatches   12;    Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           | |||||||||||:|:| |||||| || ||||||| || ||||||| |||||||
Db       1 DIQMTQSPSSLSASLGDRVIIACRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||||::||:||:||||||||||||||||  :|| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

```
RESULT 13
PL0271
Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match             78.2%;  Score 439.5;  DB 2;  Length 107;
Best Local Similarity   78.5%;  Pred. No. 2.6e-31;
Matches   84;  Conservative   10;  Mismatches   12;    Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           | ||||||| ||||:|:| |||||| || ||||||| || ||||||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDIRKMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||||::||:||:||||||||||||||||  :|| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107

RESULT 14
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ,
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones prote
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
```

```
Query Match     78.2%;   Score 439.5;  DB 1;   Length 108;
Best Local Similarity  79.4%;   Pred. No. 2.6e-31;
Matches    85;   Conservative    8;   Mismatches   13;   Indels    1;   Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||| |:|||  ||:| ||||||||: |:|||:||||: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| ||| :|||||||||||||||||| || | :|||||||||||||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107

RESULT 15
I39154
Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A;Reference number: I39154; MUID:96003804; PMID:7568160
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match     77.5%;   Score 435.5;  DB 2;   Length 108;
Best Local Similarity  79.4%;   Pred. No. 5.8e-31;
Matches    85;   Conservative    9;   Mismatches   12;   Indels    1;   Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||| |:|||  ||:| ||| |||: |:| ||:||||: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| ||||  :|||||||||||||||||| :|| | :||||||||||||
Db      61 RFSGGGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIK 107

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Job time : 9.85051 secs
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            Copyright (c) 1993 - 2003 Compugen Ltd.
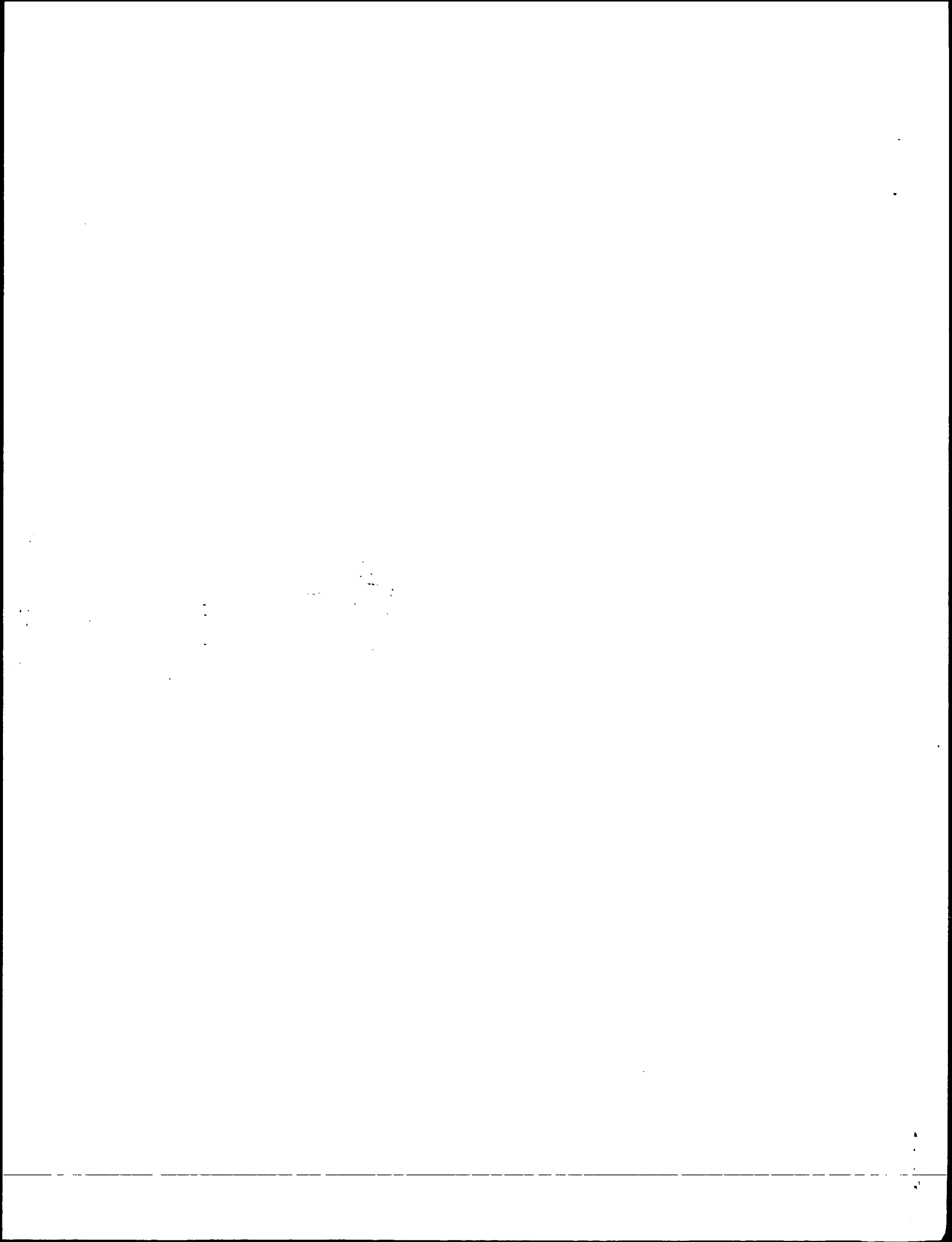
OM protein - protein search, using sw model

Run on:     January 6, 2003, 12:48:25 ; Search time 5.35354 Seconds
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                                         821.231 Million cell updates/sec

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Perfect score:  562
Sequence:       1 DIQMTQSPSSLSASVGDRVT..........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SwissProt_40:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description	
1	443.5	78.9	108	1	KV1O_HUMAN	P01607	homo sapien
2	439.5	78.2	108	1	KV1B_HUMAN	P01594	homo sapien
3	421.5	75.0	108	1	KV1M_HUMAN	P01605	homo sapien
4	419.5	74.6	108	1	KV1A_HUMAN	P01593	homo sapien
5	419.5	74.6	108	1	KV1P_HUMAN	P01608	homo sapien
6	419.5	74.6	108	1	KV1Y_HUMAN	P80362	homo sapien
7	413.5	73.6	108	1	KV1Q_HUMAN	P01609	homo sapien
8	409.5	72.9	129	1	KV1W_HUMAN	P04431	homo sapien
9	409	72.8	107	1	KV1D_HUMAN	P01596	homo sapien
10	408.5	72.7	108	1	KV1R_HUMAN	P01610	homo sapien
11	402	71.6	108	1	KV1H_HUMAN	P01600	homo sapien
12	397.5	70.7	108	1	KV1F_HUMAN	P01598	homo sapien
13	396.5	70.6	108	1	KV1K_HUMAN	P04430	homo sapien
14	390.5	69.5	108	1	KV1S_HUMAN	P01603	homo sapien
15	388.5	69.1	108	1	KV1E_HUMAN	P01597	homo sapien
16	386.5	68.8	108	1	KV1L_HUMAN	P01606	homo sapien
17	385.5	68.6	108	1	KV1N_HUMAN	P01606	homo sapien
18	384.5	68.4	108	1	KV1C_HUMAN	P01595	homo sapien
19	383.5	68.2	108	1	KV1G_HUMAN	P01599	homo sapien
20	383.5	68.2	129	1	KV1X_HUMAN	P04432	homo sapien
21	381.5	67.9	108	1	KV1S_HUMAN	P01611	homo sapien
22	376.5	67.0	134	1	KV4C_HUMAN	P06314	homo sapien
23	371.5	66.1	108	1	KV5J_MOUSE	P01643	mus musculu
24	368	65.5	117	1	KV5E_MOUSE	P01602	homo sapien
25	366.5	65.2	128	1	KV4B_HUMAN	P01637	mus musculu
26	365	64.9	133	1	KV5O_MOUSE	P06313	mus musculu
27	364.5	64.9	108	1	KV5N_MOUSE	P01648	mus musculu
28	363.5	64.7	108	1	KV1T_HUMAN	P01647	mus musculu
29	362	64.4	109	1	KV1I_HUMAN	P01612	homo sapien
30	362	64.4	117	1	KV5K_MOUSE	P01601	homo sapien
31	361.5	64.3	108	1	KV5M_MOUSE	P01644	mus musculu
32	359.5	64.0	108	1	KV5L_MOUSE	P01646	mus musculu
33	358.5	63.8	108	1		P01645	mus musculu
34	356.5	63.4	112	1	KV1U_HUMAN	P01613	homo sapien
35	348.5	62.0	114	1	KV4A_HUMAN	P01625	homo sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207	homo sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136	homo sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653	mus musculu
39	345	61.4	115	1	KV5F_MOUSE	P01638	mus musculu
40	341.5	60.8	108	1	KV5Q_MOUSE	P01650	mus musculu
41	341	60.7	109	1	KV3E_HUMAN	P01623	homo sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652	mus musculu
43	339.5	60.4	108	1	KV5U_MOUSE	P04946	mus musculu
44	339	60.3	109	1	KV3D_HUMAN	P01622	homo sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624	homo sapien

ALIGNMENTS

```
RESULT 1
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
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FT   DOMAIN        98    107       FRAMEWORK-4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE     108 AA;  11939 MW;  E801187EE6F6FB9 CRC64;

Query Match             78.2%;  Score  439.5;  DB 1;  Length 108;
Best Local Similarity   79.4%;  Pred. No. 1.1e-39;
Matches   85;  Conservative   8;  Mismatches   13;  Indels   1;  Gaps   1;

Qy          1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
               |||||||||||||||||||||| : ||||: ||| |: :|||||| |: :|:||
Db          1  DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS  60

Qy         61  RFSGSGSGGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK  106
               |||| ||:| ||||||||||||||||||| ||| : |||||||||||
Db         61  RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK  107


RESULT 3
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;    108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11834 MW;  73993A95431434A CRC64;

Query Match             75.0%;  Score  421.5;  DB 1;  Length 108;
Best Local Similarity   75.0%;  Pred. No. 8.7e-38;
Matches   81;  Conservative   11;  Mismatches   13;  Indels   3;  Gaps   2;

Qy          1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
               |||||||||||| ||||||||||||: : ||||: || |: :|||||||| ||
Db          1  DIQMTQSPSSLSVSVGDRVTITCQASQNVAYLNWYQQKPGLAPKLLIYGASTREAGVPS  60

Qy         61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK  106
               ||||||||| |:||||||||||||||||||| ||: : |||||||||:|
Db         61  RFSGSGSGIDFTFTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK  107
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FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

Query Match             78.9%;  Score  443.5;  DB 1;  Length 108;
Best Local Similarity   81.1%;  Pred. No. 4.1e-40;
Matches   86;  Conservative   9;  Mismatches   10;  Indels   1;  Gaps   1;

Qy          1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
               |||||||||||||||||||||||| ||||: ||| |: |||||||||||| || :||
Db          1  DIQMTQSPSSLSASVGDRVTIICQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS  60

Qy         61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI  105
               ||||||||| |:||||||||||||||||| ||| : ||||||||||
Db         61  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPTTFGQGTKLQI  106


RESULT 2
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;    108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; KIHUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
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RESULT 4
KV1A_HUMAN
ID   KV1A_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; KIHUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   35   49   FRAMEWORK-2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   57   88   FRAMEWORK-3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   98   107   FRAMEWORK-4.
FT   DISULFID   23   88
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match   74.6%;   Score 419.5; DB 1; Length 108;
Best Local Similarity   76.6%;   Pred. No. 1.4e-37;
Matches   82; Conservative   9; Mismatches   15; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||||| :|||| |::|||: : |:|||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||| |:||||||| :||||||||||||: ::|| ||:|:|||
Db   61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107

RESULT 5
KV1P_HUMAN
ID   KV1P_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]

RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC   MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; KIHURY.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   35   49   FRAMEWORK-2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   57   88   FRAMEWORK-3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   98   107   FRAMEWORK-4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match   74.6%;   Score 419.5; DB 1; Length 108;
Best Local Similarity   75.7%;   Pred. No. 1.4e-37;
Matches   81; Conservative   12; Mismatches   13; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||| ::||||| |:||| |::|||: : |:|||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||: |:||||||||||||||||||||||: ::|| ||| |||
Db   61 RFSGTGSG-TDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107

RESULT 6
KV1Y_HUMAN
ID   KV1Y_HUMAN   STANDARD;   PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.

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DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN         1     23       FRAMEWORK-1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        35     49       FRAMEWORK-2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        57     88       FRAMEWORK-3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN        98    107       FRAMEWORK-4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   CONFLICT      30     31       TN -> SD (IN REF. 2).
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
Best Local Similarity   75.7%;  Pred. No. 1.4e-37;
Matches   81;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||| :|||| :||  |:||| |||| |:||:| |:|
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQDITNVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         |||||||| :||||||||||||| |  |  || ||| ||| :||
Db   61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107
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RESULT 7
KV1Q_HUMAN
ID   KV1Q_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01609;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Scw.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059271; PubMed=4435756;
RA   Eulitz M., Hilschmann N.;
RT   "The primary structure of a human immunoglobulin L-chain of
RT   kappa-type (Bence-Jones protein Scw.). II: The chymotryptic peptides
RT   and the complete amino acid sequence.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01875; KIHUSW.
HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN         1     23       FRAMEWORK-1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        35     49       FRAMEWORK-2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        57     88       FRAMEWORK-3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN        98    107       FRAMEWORK-4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;  11764 MW;  32CECDDF9644414 CRC64;

Query Match             73.6%;  Score 413.5;  DB 1;  Length 108;
Best Local Similarity   74.8%;  Pred. No. 6.1e-37;
Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;
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RESULT 9
KV1D_HUMAN
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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||| :|||| ::  || |||||||||||:| :|:| |:|
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIRKHLNWYDQKPGKAPRLLIYGASTLETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         ||||||| :|||| |||||  | |:|  |  || ||| ||| :||
Db   61 RFSGSGSGTDFTLTISTLQPEDIGNYYCQQYDNVPITFGQGTRVENK 107
```

```
RESULT 8
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8501414; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; KIHUWK.
HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     22
FT   CHAIN         23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN        23     45       FRAMEWORK-1.
FT   DOMAIN        46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        57     71       FRAMEWORK-2.
FT   DOMAIN        72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        79    110       FRAMEWORK-3.
FT   DOMAIN       111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       120    129       FRAMEWORK-4.
FT   DISULFID      45    110       BY SIMILARITY.
FT   NON_TER      129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

Query Match             72.9%;  Score 409.5;  DB 1;  Length 129;
Best Local Similarity   74.8%;  Pred. No. 2e-36;
Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||  |||| :  |:|||:|||||| |||:|||||: :|
Db   23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
         ||||||| :||| ||||||||| :|||||   |  |||||||| :||
Db   83 RFSGSGSGTDFTLTISSLQPEDSAITYYCQQYSTLITFGQGTRLEIK 129
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RESULT 9
KV1D_HUMAN
```

```
ID   KV1D_HUMAN      STANDARD;      PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; KIHUAR.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Glycoprotein.
FT   CARBOHYD     28     28      N-LINKED (GLCNAC...).
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;   11703 MW;   E1BF0DF9844C3346 CRC64;

Query Match             72.8%;  Score 409;  DB 1;  Length 107;
Best Local Similarity   68.9%;  Pred. No. 1.8e-36;
Matches  73;  Conservative  20;  Mismatches  13;  Indels   0;  Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||| |||||||||| |||::||||| |||||::||: :||:|| |:| |:||
Db   1 DIQMTQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60

Qy  61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||| :||:||| ||: ||||||| ||:::||||||||
Db  61 RFSGSGSGTDFTLTISSLZPBBFATYYCQYNTFFGPGTKVDIK 106

RESULT 10
KV1R_HUMAN
ID   KV1R_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; KIHUWE.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Monoclonal antibody.
FT   DOMAIN       1     23      FRAMEWORK-1.
FT   DOMAIN      24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49      FRAMEWORK-2.
FT   DOMAIN      50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88      FRAMEWORK-3.
FT   DOMAIN      89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107      FRAMEWORK-4.
FT   DISULFID    23     88      BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11840 MW;   9249B61F0945618C CRC64;

Query Match             72.7%;  Score 408.5;  DB 1;  Length 108;
Best Local Similarity   72.0%;  Pred. No. 2e-36;
Matches  77;  Conservative  12;  Mismatches  17;  Indels   1;  Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||| |||::||||| |:||| :||: :||:||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60

Qy  61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGGGTKVEIK 106
         |||||||| :||:|| |||| |||||||:::   |||||||||:|
Db  61 RFSGSGSGTEFTLINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107

RESULT 11
KV1H_HUMAN
ID   KV1H_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; KIHUHU.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; ig; 1.
KW   Immunoglobulin v region; Bence-Jones protein.
FT   DOMAIN       1     23      FRAMEWORK-1.
FT   DOMAIN      24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49      FRAMEWORK-2.
FT   DOMAIN      50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88      FRAMEWORK-3.
FT   DOMAIN      89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107      FRAMEWORK-4.
FT   DISULFID    23     88      BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11671 MW;   08D3A6160D8D0618 CRC64;

Query Match             71.6%;  Score 402.5;  DB 1;  Length 108;
Best Local Similarity   72.9%;  Pred. No. 8.8e-36;
Matches  78;  Conservative  12;  Mismatches  16;  Indels   1;  Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||| |||::||||| |:||| :||: |:||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYILSWYQQKPGKAPQVLIYAASSLPSGVPS 60
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Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
          |||||| |:| |||||||||| ||||| : :|||||:|||||
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYITPSFGQGTRVEIK 107

RESULT 12
KV1F_HUMAN
ID   KV1F_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01866; KIHUEU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   35   49   FRAMEWORK-2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   57   88   FRAMEWORK-3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   98   107   FRAMEWORK-4.
FT   DISULFID   23   88   DISULFIDE BOND.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11788 MW;   9CD294F2F4D88823 CRC64;

Query Match   70.7%;   Score 397.5;   DB 1;   Length 108;
Best Local Similarity   70.1%;   Pred. No. 3e-35;
Matches   75;   Conservative   16;   Mismatches   15;   Indels   1;   Gaps 1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||||::||:| || ||:||||||:||||::| |:|: |:||
Db   1 DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
          |||||| |:| |||||||||| |||||||:| |||||||||:|
Db 61 RFIGSGSGTEFTLTISSLQPDDFATYYCQQYNSDSKMFGQGTKVEVK 107

RESULT 13
KV1V_HUMAN
ID   KV1V_HUMAN   STANDARD;   PRT;   108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region BAN.
OS   Homo sapiens (Human).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
DR   PIR; A01878; KIHUBN.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   35   49   FRAMEWORK-2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   57   88   FRAMEWORK-3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   98   107   FRAMEWORK-4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11840 MW;   CD3FD944FE96FD37 CRC64;

Query Match   70.6%;   Score 396.5;   DB 1;   Length 108;
Best Local Similarity   70.1%;   Pred. No. 3.8e-35;
Matches   75;   Conservative   14;   Mismatches   17;   Indels   1;   Gaps 1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||| ||||| :| :||:||||||:||||||::||:|||||
Db   1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||||| |:| |||||||||| |||||:||| :||||||||||:||
Db 61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107

RESULT 14
KV1K_HUMAN
ID   KV1K_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulin. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   35   49   FRAMEWORK-2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   57   88   FRAMEWORK-3.

```
FT   DOMAIN          89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN          98    107       FRAMEWORK-4.
FT   DISULFID        23     88       BY SIMILARITY.
FT   NON_TER        108    108
SQ   SEQUENCE       108 AA;   11900 MW;  768839FBED5A2F4B CRC64;

Query Match                      Score 390.5;  DB 1;  Length 108;
Best Local Similarity   69.5%;   Pred. No. 1.6e-34;
Matches   71;  Conservative   19;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||  ||||||||| | |:|||| ||||||::||: |:|::|| :|:||
Db    1 DIQMTQSPSTLSVSVGDRVTITCEASQTVLSYLNWYQQKPGKAPKLLIYAASSLETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        |||| ||| ||||||||:|::|| |||| : | ||||||||||::|
Db   61 RFSGQGSGTBFTFTISSV2P2BFATYYCQ2YLDLPRTFGQGTKVDLK 107

RESULT 15
KV1E_HUMAN
ID   KV1E_HUMAN    STANDARD;     PRT;    108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01865; KIHUDE.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN          1     23       FRAMEWORK-1.
FT   DOMAIN         24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN         35     49       FRAMEWORK-2.
FT   DOMAIN         50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN         57     88       FRAMEWORK-3.
FT   DOMAIN         89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN         98    107       FRAMEWORK-4.
FT   DISULFID        23     88       BY SIMILARITY.
FT   NON_TER        108    108
SQ   SEQUENCE       108 AA;   11661 MW;  BDD6E350017F1E51 CRC64;

Query Match                      Score 388.5;  DB 1;  Length 108;
Best Local Similarity   69.1%;   Pred. No. 2.6e-34;
Matches   73;  Conservative   13;  Mismatches   19;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||||||| -:|||| |||| ||||||::||| |:||:|||
Db    1 BIZMTQSPSLSASVGDRVTITCRAGQSVNKYLNWYQQKPGKAPKVLIFAASSLKSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEI 105
        |||| ||| :|:||| ||:||| ||||||: ||||||||||||
Db   61 RFSGSGSGTDFTLTISGLLPEDFATYYCQQSYTTPYTFGPGTKVEM 106

Search completed: January  6, 2003, 13:15:47
Job time : 6.35354 secs
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OM protein - protein search, using sw model

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Run on: January 6, 2003, 13:10:51 ; Search time 19.9152 Seconds
(without alignments)
1096.702 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77	Q9u177 homo sapien
2	418	74.4	241	11	Q921A6	Q921a6 mus musculu
3	414	73.7	107	4	Q96SA9	Q96sa9 homo sapien
4	406.5	72.3	108	4	Q9UL70	Q9u170 homo sapien
5	395	70.3	107	4	Q9UL81	Q9u181 homo sapien
6	385.5	68.6	108	4	Q9UL79	Q9u179 homo sapien
7	384.5	68.4	214	11	Q9R1A5	Q9r1a5 mus musculu
8	379.5	67.5	233	11	Q91WS9	Q91ws9 mus musculu
9	369.5	65.7	234	11	Q8R062	Q8r062 mus musculu
10	365.5	65.0	116	4	Q96PF6	Q96pf6 homo sapien
11	362.5	64.5	107	11	Q9JL84	Q9jl84 mus musculu
12	355.5	63.3	234	11	Q91WF8	Q91wf8 mus musculu
13	353.5	62.9	109	11	Q920E6	Q920e6 mus musculu
14	337.5	60.1	298	11	Q9QYF0	Q9qyf0 mus musculu
15	336.5	59.9	108	4	Q9UL83	Q9u183 homo sapien
16	335.5	59.7	234	11	Q8VCP0	Q8vcp0 mus musculu
17	332	59.1	109	4	Q9UL85	Q9u185 homo sapien
18	331	58.9	109	4	Q9UL78	Q9u178 homo sapien
19	329	58.5	109	4	Q9UL86	Q9u186 homo sapien
20	322.5	57.4	127	11	Q925S9	Q925s9 mus musculu
21	321.5	57.2	108	11	Q8VIJ0	Q8vij0 mus musculu
22	313.5	55.8	234	11	Q8R028	Q8r028 mus musculu
23	310	55.2	134	11	Q8VDD0	Q8vdd0 mus musculu
24	307.5	54.7	107	11	Q9ERZ9	Q9erz9 mus musculu
25	306.5	54.5	111	11	Q920E9	Q920e9 mus musculu
26	302.5	53.8	99	11	Q9JL74	Q9jl74 mus musculu
27	297	52.8	106	5	Q9U410	Q9u410 schistosoma
28	294	52.3	238	11	Q99M37	Q99m37 mus musculu
29	292.5	52.0	114	4	Q9UL80	Q9u180 homo sapien
30	284.5	50.6	101	11	Q9JL78	Q9jl78 mus musculu
31	284	50.5	235	11	Q91W12	Q91w12 mus musculu
32	281.5	50.1	97	11	Q9JL76	Q9jl76 mus musculu
33	279	49.6	239	4	Q8TCD0	Q8tcd0 homo sapien
34	278	49.5	239	11	Q8VC55	Q8vc55 mus musculu
35	277	49.3	238	11	Q8VC16	Q8vc16 mus musculu
36	273.5	48.7	109	6	Q9N0W5	Q9n0w5 oryctolagus
37	269.5	48.0	103	11	Q9JL80	Q9jl80 mus musculu
38	255	45.4	104	11	Q9JL82	Q9jl82 mus musculu
39	227	40.4	233	4	Q8TBC9	Q8tbc9 homo sapien
40	219	39.0	110	4	Q8TE63	Q8te63 homo sapien
41	216	38.4	237	4	Q8WUK4	Q8wuk4 homo sapien
42	213	37.9	237	4	Q8WTU6	Q8wtu6 homo sapien
43	212.5	37.8	107	4	Q9UL82	Q9u182 homo sapien
44	210	37.4	108	4	Q96SB0	Q96sb0 homo sapien
45	206	36.7	107	4	Q9NSD6	Q9nsd6 homo sapien

ALIGNMENTS

RESULT 1
Q9UL77
```
ID   Q9UL77       PRELIMINARY;       PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;   11738 MW;  C0668I716C4D16F3 CRC64;
```

Query Match   76.2%;   Score 428.5; DB 4; Length 108;
Best Local Similarity 76.6%;   Pred. No. 5.4e-41; .
Matches   82; Conservative   8; Mismatches   16; Indels   1; Gaps   1;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||| |||: || | : ::: |||| ||| ||| : ||:||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
```

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
         ||||||| |:| ||||||||| ||||| | |||:|||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIK 107

RESULT 2
Q921A6
ID   Q921A6;   PRELIMINARY;   PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Anti-CEA 79 single chain Fv fragment (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
DR   EMBL; U88067; AAB48044.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
FT   NON_TER   1   1
FT   NON_TER   241   241
SQ   SEQUENCE   241 AA;   26086 MW; 0276887248E9C771 CRC64;

Query Match   74.4%; Score 418; DB 11; Length 241;
Best Local Similarity   73.6%; Pred. No. 2.2e-39;
Matches   78; Conservative   12; Mismatches 16; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||:||||||||||||||||||||||||||||||||||||||:||| ||||||||||||||
Db   134 DIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSAHTLHIYIQPGIPS 193

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         ||||||||||:|:|:|||||||||| ||| ||| |||||||:||:|
Db   194 RFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLHTFGGGTKLELK 239

RESULT 3
Q96SA9
ID   Q96SA9;   PRELIMINARY;   PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB6785.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER   1   1
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA;   11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match   73.7%; Score 414; DB 4; Length 107;
Best Local Similarity   75.5%; Pred. No. 2.4e-39;
Matches   80; Conservative   9; Mismatches 17; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||:::: ||| |||:|||||||:||| |:|| |:||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         | |||||| |:| ||||||||| :| : |||||:::|||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIK 106

RESULT 4
Q9UL70
ID   Q9UL70;   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match   72.3%; Score 406.5; DB 4; Length 108;
Best Local Similarity   72.9%; Pred. No. 1.7e-38;
Matches   78; Conservative   12; Mismatches 16; Indels   0; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||:::| ||| :|| ||||||:||| |:|| |:||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         | |||||| |:| ||||||||| :| : |||||: |:||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107

RESULT 5
Q9UL81
ID   Q9UL81;   PRELIMINARY;   PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

```
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;   11501 MW;  070549FDE0754748 CRC64;

Query Match             70.3%;  Score 395;  DB 4;  Length 107;
Best Local Similarity   71.7%;          Pred. No. 3.4e-37;
Matches   76;  Conservative   10;  Mismatches   20;  Indels    0;  Gaps    0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||| || |:| |||| ||| ||: | :|| :||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||| |:+ |||| |||:| |||||||   ||| ||||:||
Db   61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106


RESULT 6
ID   Q9UL79           PRELIMINARY;       PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11787 MW;  DB5845F19724FB4E CRC64;

Query Match             68.6%;  Score 385.5;  DB 4;  Length 108;
Best Local Similarity   72.0%;          Pred. No. 4.1e-36;
Matches   77;  Conservative    8;  Mismatches   21;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        || |||||||||||||||||||| || |:|  |||| ||| :||| |||: |:|| :||
Db    1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||| |:+ |||| ||| || ||||||| |   ||||:||
Db   61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYSFPPTFGQGTKVEIK 107
```

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RESULT 7
ID   Q9R1A5           PRELIMINARY;       PRT;   214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Kappa light chain of Mab7 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER      1      1
FT   NON_TER    214    214
SQ   SEQUENCE   214 AA;   23922 MW;  52BA205FDE995E2A CRC64;

Query Match             68.4%;  Score 384.5;  DB 11;  Length 214;
Best Local Similarity   66.4%;          Pred. No. 1.2e-35;
Matches   71;  Conservative   18;  Mismatches   17;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||:|||||| ||:|||||||||||:|||:|||| ||||:|| :||| :||::||
Db    1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||| ||:| ||||: | ||:|||| ||||:|:
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107


RESULT 8
ID   Q91WS9           PRELIMINARY;       PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 25.8 kDa protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   233 AA;   25781 MW;  B1C184DA149A16EB CRC64;

Query Match             67.5%;  Score 379.5;  DB 11;  Length 233;
Best Local Similarity   69.2%;          Pred. No. 5e-35;
Matches   74;  Conservative   12;  Mismatches   20;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||| |||:|||||||||:|||:|||| |||:|| ||| :|| :||||||
Db    1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||| ||:| ||||: | ||:|||| ||||:|:
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
```

```
Best Local Similarity   66.4%;  Pred. No. 8.4e-34;
Matches  71;  Conservative  14;  Mismatches  21;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||: ||||||:||||||||||| :: ||| ||: |||:|| || : : |:: |:|:
Db    1 DIQMTQSPSSLSASVGDRVTFICQASQDIANHLNWYQKKPGEAPKFLIYDGSFLKTGVPS 60

Qy   61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||||||| ||  :: |||||||| ||||||  : |  || |||||
Db   61 RFSGGGSATNFTVTISSLQPEDFATYYCQQYHHLPFTFGPGTKVDFK 107

RESULT 11
Q9JL84
ID   Q9JL84        PRELIMINARY;        PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RL   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206022; AAF69320.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;

Query Match             64.5%;  Score 362.5;  DB 11;  Length 107;
Best Local Similarity   65.4%;  Pred. No. 1.7e-33;
Matches  70;  Conservative  11;  Mismatches  25;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||| :||| ::|| |:: |    : |||::|:|||::|:::| :||
Db    1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYTSSLXSGVPS 60

Qy   61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||||||| :: ||:::||||||||||| ||  :||  || |||:|||
Db   61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107

RESULT 12
Q91WF8
ID   Q91WF8        PRELIMINARY;        PRT;   234 AA.
AC   Q91WF8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||: ||||||:||||:|: ||| : |    : |||:: |:||||||:|:||:||||
Db   20 DIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYTSSLHSGVPS 79

Qy   61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||||||| |||:: ||:|||||||||| ||    ||  || |||:|||
Db   80 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIK 126

RESULT 9
Q8R062
ID   Q8R062        PRELIMINARY;        PRT;   234 AA.
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25857 MW;  4EB08C81426AEAB1 CRC64;

Query Match             65.7%;  Score 369.5;  DB 11;  Length 234;
Best Local Similarity   66.4%;  Pred. No. 6.9e-34;
Matches  71;  Conservative  14;  Mismatches  21;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||: ||||||:||||:|: ||| : |    : |||::|:||||||:|:||:||||
Db   21 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYTSSLHSGVPS 80

Qy   61 RFSGSGSGRDYTFISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||||||| ||:: ||:|||||||||| ||    ||  |  |||:|||
Db   81 RFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGSGTKLEIK 127

RESULT 10
Q96PF6
ID   Q96PF6        PRELIMINARY;        PRT;   116 AA.
AC   Q96PF6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Kappa 1 light chain variable region (Fragment).
GN   SDNK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21361171; PubMed=11468171;
RA   Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT   "The tropism of organ involvement in primary systemic amyloidosis:
RT   contributions of Ig V(L) germ line gene use and clonal plasma cell
RT   burden.";
RL   Blood 98:714-720(2001).
DR   EMBL; AF361758; AAK51465.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER        1      1
FT   NON_TER      116    116
SQ   SEQUENCE   116 AA;  12735 MW;  E796FC2217BFCF57 CRC64;

Query Match             65.0%;  Score 365.5;  DB 4;  Length 116;
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RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015292; AAH15292.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW   Hypothetical protein
SQ   SEQUENCE   234 AA;  25929 MW;  B0D0B0E6EB7812D2 CRC64;

Query Match             63.3%;  Score 355.5;  DB 11;  Length 234;
Best Local Similarity   64.5%;  Pred. No. 2.7e-73;
Matches   69;  Conservative   17;  Mismatches   20;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||:|||||||||:||||::|: ||||: |:||| :||||||| |:||
Db   21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
          ||||||||| :|: | |||||||: :|| ||||| |:|:|
Db   81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK 127

RESULT 13
Q920E6
ID   Q920E6           PRELIMINARY;       PRT;   109 AA.
AC   Q920E6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Pterin-mimicking anti-idiotope kappa chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307938; AAL09422.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11943 MW;  DAD3F98E05DD1501 CRC64;

Query Match             62.9%;  Score 353.5;  DB 11;  Length 109;
Best Local Similarity   61.7%;  Pred. No. 1.8e-32;
Matches   66;  Conservative   16;  Mismatches   24;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||:|||||||||||||||||:||||||:|: :|||:|| :||||
Db    1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQKQGKSPQLLVNAKTLADGVPS 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
          ||||||||| :|: | |||||:: :|| ||||| |:|:||:|||:||
Db   61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107

RESULT 14
Q9QYF0
ID   Q9QYF0           PRELIMINARY;       PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CN 8 scFv.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RX   MEDLINE=20183931; PubMed=10706631;
RA   Shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a vascular cell wall-specific monoclonal antibody
RT   recognizing a cell polarity by using a phage display subtraction
RT   method.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;

Query Match             60.1%;  Score 337.5;  DB 11;  Length 298;
Best Local Similarity   58.9%;  Pred. No. 3.9e-30;
Matches   63;  Conservative   19;  Mismatches   24;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||:|||:|||||||:||:|||::||||||||:|:||: ||||||:||| :|:||:
Db  173 DIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQGKGKSPQLLVNAKTLADGVPS 232

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
          |||||||| |: | |||||||||:|| ||: :|||:|:||:||:||
Db  233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279

RESULT 15
Q9UL83
ID   Q9UL83           PRELIMINARY;       PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

Query Match             59.9%;  Score 336.5;  DB 4;  Length 108;
Best Local Similarity   60.2%;  Pred. No. 1.5e-30;
Matches   65;  Conservative   17;  Mismatches   23;  Indels   3;  Gaps   2;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ::|||||:|||||||||||||||||||||||||||:|: |||||::|||
Db    1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
          |||||||| |: | |||||:: :||: |:|: | ||
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Db   61 RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107

Search completed: January 6, 2003, 13:17:28
Job time : 20.9152 secs